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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                               Database
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                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                            987554321
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23
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    Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                       13736207 seqs, 6748477542 residues
                                                                                                                                                                                                              EST: *
                                                                                                                                                                                                                                                                   Minimum Match 0%
                                                                                                                                                                                                                                      Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                          em_htc:*
gb_est1:*
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em_gss_pln:*
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(without alignments)
256.813 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 17	16	c 15	c 14	c 13	c 12	c 11	10	9	0	c 7	0	G 5	0 4	w	2	c 1	NO.	Donati I +
16.8	16.8	17	17	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.4	17.4	17.8	17.8	18.2		Score	
73.0	73.0	73.9	73.9		74.8			74.8		74.8	75.7	75.7	77.4	77.4	79.1	79.1	Match Length	
346	325	520	476	1302	997	632	574	475	455	246	511	401	697	375	914	530		
9	9	10	10	10	12	10	12	10	9	10	10	10	10	Ø	10	12	DB	
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16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6		16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6		16.6	16.8	16.8	16.8	16.8	16.8	16.8	
72.2	72.2			72.2	72.2	72.2	72.2			72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	73.0	73.0	73.0	73.0	73.0	73.0	
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AZ222176	AZ574567	AZ115664	BM426935	AQ984457	AW934499	AZ093474	AU145954	в68429	BH403758	BE450880	TA391F03Q	BF768721	AQ550432	AA922286	BF036944	AZ058336	BF765798	вн376297	BB308471	вв369390	BF237879	BF204564	BI086804	AW057195	AI940638	AI940637	
AZ222176 RPC1 23 6	AZ574567 33019B10	AZ115664 RPCI-24-1	BM426935 pqf2n.pk0	AQ984457 RPC1-23-3	AW934499 EST 353403	AZ093474 KPC1-23-	AU145954 AU145954	868429 C11-HSF 2#2	BH403758 AG-NI-131	BE450880 ES1401767	AL498362 1. brucei	BF768721 QV3-11000	AQ550432 KPC1-11	AA922286 om46h06.s	BF036944 6d1459]73	AZ058336 KPC1-24-	BF765798 11.2 CSOU4	BB376297 BB376297	BB308471 BB30847	BB369390 BB369490	BF237879 601842442	BF204564 60186817	BI086804 602850413	AW057195 canzans,y	A1940638 IL+ S1002	A1940637 11.4-Slenz	

ALIGNMENTS

FEATURES ACCESSION VERSION RESULT 1 AQ457613/c COMMENT REFERENCE SOURCE DEFINITION KEYWORDS ORGANISM MEDLINE TITLE JOURNAL AUTHORS source Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostowi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 530)

cmith K Swartzell.S., Holzman, I., library availability, please contact Pieter de Jong (pieter deejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 673 row: P column: 13 High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA Tel: (206) 616-3618
Fax: (206) 616-3887 AQ457613 530 bp 'DNA linear GSS 23-APR HS_5097_B1_H07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-673 CoJ-13 Row-P, DNA sequence. High quality sequence stop: 530. Plate: 673 row: Seq primer: T7 Class: BAC ends 99380589 Contact: Mahairas GG, Wallace JC, Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) GSSEmail: jwallacetu.washington.edu Clones are derived from the human BAC library RPC1-11. For BAC Hood, L Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and human. AQ457613.1 GI:4636253 AQ457613 /organism="Homo sapiens" . 530 T pooH 98109, USA GSS 23-APR 1999

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SOURCE
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98
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                                       1 ACCACGACTGAGCACGCACCTTT 23
ACCAAGACTGAGGACGCACCCTT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
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1 (bases 1 to 914)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
Plate: LLAM10244 row: t column: 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: eqapbs-remail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution intormation can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Lite Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
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                                                                                         ('onservative
                                                                                                                                                                                                     /clone_lib="NHH_MGC_89"
/tissue_type: "hypernephroma, cell line"
/lab_bost="bH108 (phage-resistant)"
/note="Organ: kidney: Vector: pCMV-SPORP5; Site_1: Not1;
Site_2: Salf; Cloned unidirectionally; oliqo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologics.
Note: this is a NHH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex "male"
/note "Vector: pBACe3.6; Site_1: Ecok1; Site_2: Ecok1;
/note "Vector: pBACe3.6; Site_1: Ecok1; Site_2: Ecok1;
Male blood DNA was isolated trom one randomly chosen donor
and partially divested with a combination of Ecok1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECORI Methylase. Size selected DNA was cloned into the pRACE3.6 vector at EcoRI sites"
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/clone."Plate 673 Col.13 Row P"
/clone_lib_"RPCI-11 Buman Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/cione="!MAGE:4453640"
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                                                                                  79.1%; Score 18.2; DB 10; 87.0%; Pred. No. 4.3e+02; tive 0; Mismatches 3;
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Smith, r.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Steher, F.L.,
Gasas, E., Wray, J.E., White, J., Cho, J., Fabrenktud, S.C., Rennett
G.L., Heaton, M.P., Lacqueid, W.W., Robrer, G.A., Chitko McK. Was, Cit.
Pertea, G., Holl, L., Karamycheva, S., Liana, F., Quackenbush, J. and
Keele, J.W.
                Enkaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                 EST.
                                                                                                                                                                           sequence.
BI875875
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[164b07.yl Sugano Kawakami zebratish DRA Danio rerio cUNA clone
3818460 5' similar to Tk:029517 Q29517 PHOSPHOLIPASE C ;, mRNA
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Fo Box 166, Clay Center, NE 68943-0166, USA
                                                                                  Danio rerio
                                                                                                                                                      в1875875.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing, Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the mins one 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
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Mammalia; Entheria; Cetartiodaetyla; Ruminantia; Pecora; Bezondea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW478086.1 G1:7048192
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                                                                                                            zebratish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith*email.marc.usda.qov
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(bases 1 to 697)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note "Vector: pCMV SPORT6: Site_1: Xhal: Site_2: Xhal: Library made from pooled tissue from lymph node, ovary. fat, hypothalamus, and pitultary."

122 c 101 g 88 t
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/db_xret "taxon:9913"
/clone_lib-"MARC 1BGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host "DH10B"
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                      McCarter, J., Clifton, S., Chiapolli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maquire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                  rr16e10.yl Globodera rostochiensis J2 pcDNAII Smant v1 Globodera rostochiensis cDNA 5' similar to TR:Q18231 Q18231 SIMILAR TO 40S RIBOSOMAL PROTEIN S30/UBIQUITIN-LIKE PROTEIN. [1] :, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consortium/LLNL, send email to: info@image.lHnl.gov High quality sequence stop: 520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library constructed by Dr. Sumio Sugano and Dr. Kolchi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone
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Fax: 314 286 1810
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                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadoroa; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                                                                                                                                                                               Globodera rostochiensis.
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Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                (bases 1 to 401)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Kolchi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTGCTGTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [TGTTGGCCTACTGG], digested and cloned into distinct Drall1 sites of the pME188-FL3 vector (5' site CACTGTGTGTG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pME18S-F13; Site_1: Drail! (CACTGTGTG); Site_2: Drail! (CACCATGTG); 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH108 (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex-"mixed (one male and one female, including unfertilized eggs)"
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/strain="AB"
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90.5%;
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JOURNAL
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Best Local Similarity
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Globodera rostochiensis
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Contact: McCarter JP
                                                                                                               The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
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Wishington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu The library was contributed by Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999
                  Email: estewatson.wustl.edu
The library was contributed by Dr. Geert Smant of the Laboratory of
                                                                                                                                                                                             Unpublished (1999)
Contact: McCarter JP
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                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                          Wilson, R.
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Nematology at Wageninden University, Wageningen
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                                                                                                                                                                                                                                                                                               Shin,
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M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
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Nematology, The Netherlands."
a 58 c 80 g 62 t 1 others
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/db_xre1-"taxon:31243"
/ctone_lib="Globodera rostochiensis J2 pcDMAII Smanc
/dev_stage-"J2"
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94.7%;
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Pred. No. 7.3e+U2;
"" mmatches 1;
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                                                                                                                       St. Louis, MO 63108, USA
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Nethorlands(geert.smant@nema.dpw.wau.nl). DNA Washington University Genome Sequencing Center

DNA Sequencing by

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12484 MVA14 bloodStream form of serodeme WKATall. Trypanosomu
brucel rhodesionse cDNA 5', mkNA sequence.
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Trypanosoma brucei rhodesiense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: p.majiwa@cgnet.com
Seq primer: T3 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.O. Box 30709, Nairobi, Kenya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular Biology Unit
International Livestock Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Majiwa PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation of expressed sequence tags as physical landmarks in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Djikeng, A., Dönelson, J.E. and Majiwa, P.A.O
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/note "Vector: pcDNMII (Invitrogen): Site_1: BstXI;
/note - Zite_1: Bs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:31286"
/clone_lib="MVAT4 bloodstream form of serodeme MRATatl.!"
/note-"Vector: Lambda ZAP 11 (Stratagene); Site_t: Ecort;
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/dev_stage "J2"
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/db_xrei-"taxon:31243"
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                                                                                                                                                            74.8%;
86.4%;
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                                                                                                                                                            Score 17.2; DB 16
Pred. No. 7.6e+02;
                                                                                                                              Mismatches
                                                                                                                                                                                       DB 10; Length 246;
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374175 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Cetartiodaetyla; Suina; Suidae; Sus. 1 (bases 1 to 475)
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1 (bases 1 to 455)
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eDNA Library Preparation: M. Hento Soares, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lemon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   this DNA was used as tracer in a subtractive hybridization reaction. The driver was FCM-amplified cDNAs from a paol of 5,000 clones made from the same library clonells 1257096-1258641, 1469064-1470983, and 1475592-1470743). Subtraction by Bento Soares and M. Fatima Bonaldo. " 148 g 88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polylinker, site 1: Not 1: Site 2: Eco RI, Flasmid DNA
from the mormalized library NCL_CAP_GCA was prepared, and
ss circles were made in vitro. Following HAP purification.
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/lab_host="DH108"
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/clone-"1MAGE:2237197"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"NCI_CGAP_GC6"
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86.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                            Stanford University
855 California Ave, Palo Alto,
Tel: 650 725 8221
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 6893-0166, USA
                                                                                                                                                                                                                                                                                                                                              clade; Panicoideae; Andropogoneae; Zea. l (bases 1 to 574)
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH622013 574 bp DNA linear GSS 10-1007116B04.x1 1007 - RescueMu Grid H Zea mays genomic, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith/comail.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
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                                                                                                   Reverse complemented post-ligation
                                                                                                                                                                                                                                             Department of Biological Sciences
                                                                                                                                                                                                                                                                  Contact: Walbot V
                                                                                                                                                                                                                                                                                   Unpublished (200)
                                                                                                                                                                                                                                                                                                      Maize genomic sequences found using engineered RescueMu transposor
                                                                                                                                                                                                                                                                                                                             Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 402 752 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST discovery in swine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        St.one, R. F.,
                                                                                                                  Possible ligation site of ends cut by 2 different endonucleases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
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                                                           transposon-tagged
                                                                                                                                           walbot@stanford.edu
                                                                                1007116 column: 24
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/organism="Zea mays"
                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MARC 2PIG"
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                                                                                               sequence from source sequence
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Ouery Match 74.8%; Score 17.2; DB 12; Best Local Similarity 86.4%; Pred. No. 1e-03;
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ZP637-1-000863 Zebrafish shield stage whole embryo chNA library
MPMCp637 Danio rerio chNA clone MPMCp637_16812;MFMCp637E1216-57.
                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Max-Planck-Institut fuer Molekulare Genetik
Ihmestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1512
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Hennig S
laboraty 123, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H. EST sequencing of a zebrafish shield stade cDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio
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                                                                                                                                                                                     /db_xref~"taxon:7955"
/clone-"MPWGp637_16E12;MPMGp637E1216"
/clone_lib-"Zebrafish shield stage whole embryo cDNA
/blone_"MPMGp637"
/blone_""."
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/db_xref-"taxon:4577"
/clone_lib-"1007 - kescueMu Orid H"
                           /note="Vector: pSportl; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-morgan: leat; Vector: Resemblu (endineered from
pBlueScript backbone); Site_1: BamHI; Site_2: Bqill:
RescueMu is a 4.9 kb, modified maize Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type:"leat"
/dev_stage:"adult"
library normalised by oligonucleotide fingerprinting"
                                                                                          /tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 blue MRF"
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601656421R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856229 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                            Smith.T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone, R.L., Casas,B., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett, G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UP Tel: 402 762 4366
                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine CDNA
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National Institutes of Health, Mammailan Gene Collection (MFT)
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                                                                                                                                                                                                                                                                                                    Keele, J.W.
                                                                                                                                                                                                                                                                                                                                    Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 476)
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//lab_nost="bH108 (phage-resistant)"
/note="Organ: ovary; Vector: pcMV-SPORT6; Site_1: Not1;
/note="Organ: ovary; Vector: pcMV-SPORT6; Site_1: Not1;
/note="Organ: ovary; Vector: pcMV-SPORT6; Site_1: Not1;
/note="Technologies"
/note="contact size 1.8 kb. Library constructed by lite
/note-freehoologies."
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/clone_lib="NIH_MGC_66"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 65 row: P column: 12
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smitheemail.marc.usda.dov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
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Seg primer: ATTTAGGTGACACTATAG.
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Tel: 301 504 8416
Fax: 301 504 8414
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                                                                                                                                                                                                                                                                                                          Email: tads@lpsi.barc.usda.qov
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                      /organism="Bos taurus"
/db_x(ef."taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref-"taxon:9913"
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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Xho1;
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                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                accacgactgagcacgcaccttt 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version Copyright (c) 1993 - 2002
                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Search time 148.222 Seconds
(without alignments)
266.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compugen Ltd
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								a	No.
9 16.6	3 16.6	7 16.6	5 16.6	5 16.6	4 16.6	3 16.6	2 16.6	1 16.6	Score
72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	Match Length DB ID
2319	1693	1181	1181	809	787	736	736	574	Length
23	22	22	20	20	20	20	20	22	DB
AAS91632	AAH13873	AAS09902	AAX27502	AAV69440	AAV69442	AAV69443	AAV69441	AAH09581	ID
DNA encoding nove	Human cDNA sequenc	DNA encoding ethy	Banana ethylene-1	Banana fruit ripe	Banana fruit ripe	Banana fruit ripe	Banana fruit ripen	Human cDNA clone	Description

							C		O			C											С				C							a	
45	44	<u>ا د</u>	4 2	41	40	39	38 8	37	36	35	34	W	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
	J (n (15.6	лi		Çn.	15.6	ŗ	S,	15.6	5	5	ŭ,	5	5	5	5	Ģ	.5	5	5	5	15.8	5	5		Š	U		5		σ.		16.6	16.6
67.8											,	٠											68.7	•	•		•			•		•	72.2	2	72.2
3237																				5684	3608	2643	1552	972	932	828	828	380	2990	2510	744	14872	10079	10079	10079
24																																	Ñ		_
ABA04065	ABA04062	7904044	ABA04068	ABA04069	ABL27646	ABL26239	AAH17346	AAH48496	AAH04495	AAS21884	ААН93954	AAC98099	AAS91030	ABL27647	AA254158	AA254157	AAV96124	AA163610	AAI99260	AAC59953	ABL05192	AAH33383	ABL05193	AAS85277	AAI58150	AAK65952	AAK65951	AAV88222	ABL27152	ABL27146	ABL27153	AAV52205	AAA28294	ω	AAQ88057
-	Human semaphorin G	0 0 0	sema	Human semaphorin G		Drosophila melanog	Human cDNA sequenc	Japanese medaka fe	Human cDNA clone (Human collagen gen	Human foetal coNA,	Human colon cancer	DNA encoding novel	Drosophila melanog	Neisseria meningit	Neisseria meningit	Solanidine glucosy	Human kidney relat	Human excretory re	Human secreted pro	Drosophila melanog	Human colon cancer	Drosophila melanog	DNA encoding novel	Human polynucleoti	Human immune/haema	Human immune/haema	EST clone DX295.		Drosophila melanog	Drosophila melanog	Streptococcus pneu	Human superoxide d	Human EC-SOD gene.	Human EC-SOD gene.

ALIGNMENTS

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RESULT 1
AAH09581/c
 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                 Ota T, Ishii S,
WPI; 2001-318749/34.
                                                                09-JUN-2000;
                                                                                                                                        07-FEB-2001.
                                                                                                                                                           EP1074617-A2.
                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                               Human cDNA clone (3'-primer) SEQ ID NO:6416.
                                                                                                                                                                                                                                                      AAH09581;
                                                                                                                                                                                                                                                                      AAH09581 standard; cDNA; 574
                                             (HELI-) HELIX RES INST.
                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                   26-JUN-2001 (first entry)
                Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                              ; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                     99JP-0248036
                                                                                                                                                                                                                                                                        ₽P
                Hayashi K, S
A, Nagai K,
                 Saito K, Yamamoto J;
, Otsuki T;
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SS

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209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 1s elected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13628 and AAH313633 to AAH4242 represent human cDNA sequences; AAB92446 to AAH3693 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present
full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                       WPI; 1999-059745/05
                                                                                        Bird CR,
                                                                                                                      (ZENE ) ZENECA LTD
                                                                                                                                                                                          05-MAY-1998;
                                                                                                                                                                                                                          26-NOV-1998
                                                                                                                                                                                                                                                          WO9853085-A1
                                                                                                                                                                                                                                                                                            Musa acuminata
                                                                                                                                                                                                                                                                                                                                           Fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                          Banana fruit ripening-related clone U-13 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV69441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV69441 standard; cDNA; 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                            triploid; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCACGACTGAGCACGCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCACGCCCGATCACGCACCTCT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574 BP; 118 A; 144 C; 162 G;
                                                                                     Medina-Suarez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID 6416;
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                        97GB-0010370
                                                                                                                                                                                        98WO-GB01297
                                                                                                                                                                                                                                                                                                                            breeding; ss.
                                                                                                                                                                                                                                                                                                                                        banana; modulator; tissue senescence; crop; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2537pp + CD ROM; English
                                                                                     RDJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.6; µ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                     Seymour GB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Matches Query Match

Conservative

0;

Mismatches

4.

0;

Gaps

0;

72.2%; 82.6%;

Pred. No.

Score 16.6;

DB

20;

Length Indels

736;

Best Local Similarity

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RESULT 3
AAV69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                           New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening characteristics
                                                                                                                                                                                                                                                           Bird
                                      globally important crop. In particular, the method can \mathfrak n characteristics in the dessert banana, which due to its
                                                   modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such
                                                                              modulate the fruit ripening or tissue senescence characteristics of Musa acuminata (banana) plants. The method provides a recombinant way of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              globally important crop. In particular, the method can modulate such characteristics in the dessert banana, which due to its triploid nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulate the fruit ripening or tissue senescence characteristics of Musa acuminata (banana) plants. The method provides a recombinant way of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in processes for modifying plant/fruit ripening characteristics
  Sequence
                           is unaffected by
                                                                                                         AAV69440-V69512 are cDNA sequences which are used in a method
                                                                                                                                    Claim 1; Page 20; 78pp; English
                                                                                                                                                                                                                                 WPI; 1999-059745/05
                                                                                                                                                                                                                                                                                                                20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                      26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                 WO9853085-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           Musa acuminata
                                                                                                                                                                                                                                                                                                                                                                                                                                                   triploid; plant breeding; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banana fruit ripening-related clone U-105 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV69443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV69443 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is unaffected by conventional plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating ripening/senescence characteristics of bananas, which are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV69440-V69512 are cDNA sequences which are used in a method to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                                                                                                                                                            CR, Medina-Suarez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTCGACTGGGAAAGCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
19; Conser
 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 BP; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                97GB-0010370
                                                                                                                                                                                                                                                                                                                                           98WO-GB01297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 banana; modulator;
 189
                           conventional plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.2%;
A; 193 C; 202 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 190 C; 196
                                                                                                                                                                                                                                                            RDJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.6; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
                                                                                                                                                                                                                                                         Seymour GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 146 T;
138 T; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                techniques
                         techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crop; plant;
                                       triploid nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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23

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RESULT 5
AAV69440
  KW XXX DXX
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                                                                                                                                                                           g
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                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                         modulate the fruit ripening or tissue senescence characteristics of Musa acuminata (banana) plants. The method provides a recombinant way of modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such
                                                                                                                                                                                                                                                                                                                                                                                                                                        New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Banana fruit ripening-related clone U-23 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV69442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV69442 standard; cDNA; 787
Fruit ripening;
triploid; plant
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 19-20; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09853085-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Musa acuminata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              triploid; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1999
                                   Banana fruit ripening-related clone U-7 cDNA
                                                             15-MAR-1999
                                                                                                             AAV69440 standard; cDNA; 809
                                                                                                                                                                                                                                                                          Sequence 787 BP; 209 A; 206 C; 216 G; 150 T; 6 other;
                                                                                                                                                                                                                                                                                                             characteristics in the dessert banana, which due to its triploid nature
                                                                                                                                                                                                                                                                                                                                                                              AAV69440-V69512 are cDNA sequences which are used in a method to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-059745/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284
                                                                                                                                                                          284
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                 1 ACCACGACTGAGCACGCACCTTT
                                                                                                                                                                                                                                                                                                   unaffected by conventional plant breeding techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCGACTGGGAAAGCACCTTT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCACGACTGAGCACGCACCTTT
                                                                                                                                                                          ACCTCGACTGGGAAAGCACCTTT 306
                                                                                                                                                                                                                          l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medina-Suarez RDJ,
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-0010370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-GB01297
banana; modulator; tissue senescence; crop; plant;
breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          banana; modulator; tissue senescence; crop; plant;
                                                                                                                                                                                                                                     72.2%;
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВÞ
                                                                                                             ΒP
                                                                                                                                                                                                 23
                                                                                                                                                                                                                                      Pred. No. 82;
                                                                                                                                                                                                                                                   Score 16.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seymour GB;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                   DВ
                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                 787;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                        0
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RESULT 6 AAX27502

AAX27502;

26-MAY-1999

(first entry)

AAX27502 standard; cDNA; 1181 BP

23-MAR-1999 US5886164-A

WPI; 1999-228611/19

Bird CR,

Fletcher JD;

(ZENE) ZENECA 15-APR-1996; 15-APR-1996;

LTD.

96US-0632598

96US-0632598

1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana; ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening; transgenic; enzyme; inhibition; flavour; texture; ss.

Banana ethylene-forming enzyme cDNA sequence

밁

277

ACCTCGACTGGGAAAGCACCTTT 299

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Qγ
                        Query Match
Best Local S
Matches 19
                                                                                                               AAV69440-V69512 are cDNA sequences which are used in a method to modulate the fruit ripening or tissue senescence characteristics of Musa acuminata (banana) plants. The method provides a recombinant way of modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such characteristics in the dessert banana, which due to its triploid nature
                                                                                                                                                                                                                                      New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening characteristics
                                                                                                                                                                                                            Claim 1; Page 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Musa acuminata
                                                                             Sequence
                                                                                                                                                                                                                                                                                                        WPI; 1999-059745/05
                                                                                                                                                                                                                                                                                                                                  Bird CR,
                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9853085-Al.
                                                                                                       is unaffected by
                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA
                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1997;
                          Local Similarity
les 19; Conser
ACCACGACTGAGCACGCACCTTT 23
                                                                             809 BP;
                                                                                                                                                                                                                                                                                                                                  Medina-Suarez RDJ,
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                     97GB-0010370
                                                                                                                                                                                                                                                                                                                                                                                                              98WU-GB01297
                                                                           210 A; 214 C; 217
                                                                                                    conventional plant breeding techniques
                                   72.2%;
                          0;
                                   Pred.
                                     Score 16.6;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                  Seymour GB;
                          Mismatches
                                                                             <u>.</u>
                                                                          153 T; 15 other;
                                     82;
                                                    DB
                                                   20;
                          Indels
                                                 Length 809;
                          0;
                          Gaps
                                                                                                                                                                        Musa
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respectived, pASC6 and pACCS7 may be used to genetically control ethylene biosynthesis in plants and hence regulate the ethylene-induced processes involved in fruit ripening (and other ethylene related processes). Vectors comprising the cDNA sequences may be used to produce transgenic bananas with altered fruit ripening characteristics. The crientation of the pASC6 and pACCS7 used in the construct, will determine how the ripening process is affected. If the genes have a sense orientation, and transcribe mRNA that encodes an active enzyme, the rate of ripening will be increased (up-regulation) (however, full-length sense constructs can also be used to inhibit enzyme expression by conhibition). If genes encode antisense mRNA, they will inhibit the expression of the genes involved in fruit ripening and hence slow the process down (down-regulation). In this manner different spatial and the process down (down-regulation). In this manner different spatial and the process down (down-regulation). In this manner different spatial and
          Modifying level of ethylene biosynthesis in plant of genus Musa
                                                                         WPI; 2001-450497/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rate of ripening will reduce the rate of deterioration of banana fruit after harvest. This helps in production of high quality fruit that has improved flavour and texture. The present sequence represents the cDNA sequence of the banana BFE enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (pACOS7)) encoding 1-aminocyclopropane-i-carboxylic acid synthase and an ethylene forming enzyme (EFE), respectively. The clones are deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814,
                                                                                                                           Bird CR,
                                                                                                                                                                                                                                                                                                                          17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit storage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana;
ethylene blosynthesis; ethylene-forming enzyme; EFE; fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding ethylene-forming enzyme (EFE) from banana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS09902 standard; cDNA; 1181 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated cDNA molecules ((pASC6) and (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene forming enzyme (EFE) - useful for modifying truit ripening
                                                                                                                                                                                                                         15-APR-1996;
                                                                                                                                                                                                                                                                        15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                            US6262346-Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        temporal patterns of genes expression can be produced. Retardation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to two isolated cDNA molecules ((pASC6) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTCGACTGGGAAAGCACCTTT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Columns 13-14; 22pp; English.
                                                                                                                     Fletcher JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS
                                                                                                                                                                                                                         96US-0632598
                                                                                                                                                                                                                                                                        9908-0231240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       especially in bananas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 A; 294 C; 318 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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QY

involves inserting into

genome of plant a DNA sequence encoding banana

Claim 8; SEQ ID 10870;

2537pp + CD

ROM; English

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RESULT 8
AAH13873
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                     11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                       Primer sets for synthesizing polynucleotides, particularly the full-length cDNAs defined in the specification, and for the det and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in good condition. In this way high quality ripe fruit can be made available to the consumer with reduced requirement for post-harvest treatment. High quality fruit will have improved flavour and texture. High quality fruit can be produced consistently over a wide harvest period, and such fruit can be held in store for long periods and ripened to optimal quality by the supply of exogenous ethylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an ethylene-forming enzyme (EFE), where (I) is in sense or antisense configuration, and modifies the level of activity of ACS or EFE. This retards the rate of ripening in banana fruits which reduces the rate of deterioration of banana fruit after harvest. As a result, fruit may be harvested when they have reached partial or full ripeness and still have the robustness to withstand handling and transport to reach the consumer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genus Musa by inserting into the genome of the plant a DNA sequence (1) encoding a banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) or
                         full-length cDNAs
                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                      07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:10870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming
                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH13873 s....dard; cDNA; 1693 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the coding sequence of ethylene-forming enzymo
                                                                                                                                Ishii
                                                                                                                                                                         (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       involves modifying the level of ethylene biosynthesis in a plant of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 ACCTCGACTGGGAAAGCACCTTT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                              Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Column 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from banana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                        HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                              Isogai T,
                                                                                                                           sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                     2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP;
                                                                                                                                                                                                                                                  99JP-0300253
                                                                                                                                                                                                                                                               99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 A; 294 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the method of the invention. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%;
82.6%;
                                                                                                                              Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                             Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>,</del>
                                                                                                                              Saito K,
(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                              7
                                                                                                                                           Yamamoto
                                       by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                      detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0

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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3533 to AAH18742 represent human cDNA sequences; and AAH3629 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-df primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
           Claim 1; SEQ ID No 27436; 103pp; English
                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess bidinostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1382 ACCACGCCCGATCACGCACCTCT 1404
                                                                                                                                                     WPI: 2001-639362/73.
                                                                                                                                                                                          Drmanac RT,
                                                                                                                                                                                                                              (HYSE-)
                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                         W0200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #27436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS91632 standard; cDNA; 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1693 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                      P-PSDB; ABG27445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCACGACTGAGCACGCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
19; Conserv
                                                                                                                                                                                                                              HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 A; 531 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 10
AAQ88057/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino aci; sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from Wilming the first the first of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quantitating a polypeptide in tissue, as molecular weight markers and at a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tays for identifying expressed genes. (I) is useful in gene therapy techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 ACCACGCCCGATCACGCACCTCT 1043
                    misc_signa
                                                                                                                                                                                                                                                                          misc_signal
                                                                                                                                                                                                                                                                                                                                                          misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human EC-SOD gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2319 BP; 501 A; 799 C; 642 G; 377 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                    misc_signal
                                                                                                                                                                                       misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EC-SOD; superoxide dismutase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ88057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ88057 standard; DNA; 10079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
121..126
                 complement (251..256;
                                                                                                                                                                                       /label= metal regulatory element 650..660
                                                                                                                                                                                                                                                                                                                                                             1085..1090
                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (238..244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (370..375)
/*tag= c
                                            /label= antioxidant response element
                                                                                                                         /*tag= g
/label= antioxidant response element
                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                  /label= xenobiotic responsive element
                                                                                                                                                                                                                                                                                                                                                                                     /label= trans-activating factor response element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= glucocorticoid response element halfsite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= cAMP responsive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5085..5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.2%;
82.6%;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.6;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as
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RESULT 11
AAT92317/c
ID AAT9231
XX AC AAT923
XX OAT923
XX

AC AAT923
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AC AAT92
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AC AAT923
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AC AAT92
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crapo JD,
                                                     Oxidant scavenger; extracellular matrix targetting moiety; cell surface matrix; nitrogen containing macrocyclic moiety; inflammatory condition; aberrant smooth muscle function; ischaemia reperfusion injury; myocardial infarction; stroke; acute head trauma; organ reperfusion; bowel ischaemia; pulmonary infarction; glaucoma; EC-SOD; superoxide dismutase; tetrameric glycosylated copper and zinc containing enzyme; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1238 ACCTCAACTTAGCACCCACCTTT 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone 7 from a human adult leukocyte genomic library was analysed. The analysis revealed that human EC-SOD contains three exons and two introns. The intron-exon boundaries are shown in AAQ88062-Q88065 AAQ88057 shows the entire sequence for the human EC-SOD gene. Exon 3 contains the entire uninterrupted coding region. An obviour TATA box cannot be discerned for the EC-SOD gene. Two CAAT box elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were identified. One is in the reverse orientation and located about 20bp upstream of the first exon. Transcriptional factor database searching of the 5'-nontranslated region and first exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Super:oxide dismutase mimetic(s) comprising a nitrogen-containing macrocyclic moiety - useful in treatment of inflammation, musculature disorders, atherosclerosis or gout.
               Homo sapiens
                                                                                                                                                                                                                                                     Human EC-SOD gene
                                                                                                                                                                                                                                                                                                        06-FEB-1998
                                                                                                                                                                                                                                                                                                                                                        AAT92317;
                                                                                                                                                                                                                                                                                                                                                                                                        AAT92317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10079 BP; 2482 A; 2613 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 33; Figure 24; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-161483/21.
P-PSDB; AAR72413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09510185-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enhancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYAL-) UNIV ALABAMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 revealed several potential regulatory elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Folzrj;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Day BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0136207
94US-0136207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US11558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= SV40 enhancer region AP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= AP1
171..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= sis responsive element
162..168
                                                                                                                                                                                                                                                                                                                                                                                                   CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                   10079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.6; [Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Freeman BA,
                                                     zinc containing enzyme; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2407 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site/TPA responsive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fridovich I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2577 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see FT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
       ID XX AC AC DT DT
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                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
Human superoxide dismutase (EC-SOD) gene.
                                                                                                                                                                                                                                                                       1238 ACCTCAACTTAGCACCCACCTTT 1216
                                                  12-FEB-2001 (first entry)
                                                                                                     AAA28294;
                                                                                                                                                AAA28294 standard; DNA; 10079
                                                                                                                                                                                                                                                                                                1 ACCACGACTGAGCACGCACCTTT 23
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QΥ

Indels

Gaps

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                              biological processes involving oxidants. They can be used for e.g. treating inflammatory conditions, treating disorders resulting from aberrant smooth muscle function or to protect against ischaemia reperfusion injuries associated with myocardial infarction, stroke, acute head trauma, organ reperfusion following transplantation, bowel ischaemia, pulmonary infarction, surgical occlusion of blood flow, and soft tissue injury. They can further be used to protect against damage to the eye due to sunlight (and to the skin) as well as glaucoma, and macular degeneration of the eye. Diseases of the bone are also amenable to treatment with the compounds, and connective tissue disorders
                                                                                                                                                                                                                                    treated with the compounds. In the oxidant scavengers, substituents can be selected to render them resistant to degradation by haemoxygenase and also so that they do not interfere with normal porphyrin metabolism, can pass through cell membranes and bind to cell surface or extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a tetrameric glycosylated copper and zinc containing superoxide dismutase enzyme. The oxidant scavengers can be used for protecting against the deleterious effects of oxidants and for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macrocyclic moiety and a cell surface or extracellular matrix targetting moiety, or their salts. The present sequence encodes the human EC-SOD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New porphyrin-type oxidant scavengers - used for protecting against oxidants and for modulating biological processes involving oxidants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Batinic-Haberle I, (Fridovich I, Oury T,
                                                                                                                                 Sequence 10079 BP; 2481 A; 2612 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidant scavengers have been developed comprising a nitrogen containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW32599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9640223-A1
                                                                                                                                                                                                                                                                                                                                                                         associated with defects in collagen synthesis or degradation can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TROV/) TROVA M P.
(UYAL-) UNIV ALABAMA
Local Similarity 82.6 hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-077220/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0613418
95US-0476866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 5085..5807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crapo JD,
                            72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trova MP;
0;
                                   Score 16.6;
Pred. No. 1
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   Mismatches
                                                                                                                                 2409 G; 2577 T; 0 other;
                               1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folz RJ,
                                                                  DB 18;
                                                           Length 10079;
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0;
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15-OCT-1993;
13-OCT-1994;
07-JUN-1995;
11-MAR-1996;
                      hypertension, artherosclérosis, oedema, septic shock, pulmonary hypertension, impotence, infertility, endometriosis, premature uterine contractions, microbial infections, gout, Type II diabetes meilitus, inflammation of the lungs, asthma, pneumonia, cystic fibrosis, chronic sinusitis and autoimmune disease. The present sequence represents the
                                                                                                                                                                                                                                                                                  bones, to increase the limited storage viability of transplanted hearts, kidneys, skin and other organs and tissues. The compounds are also useful in the treatment of diseases of the central nervous system (including AIDS dementia, stroke, amylotrophic lateral sclerosis), Parkinson's disease, Huntington's disease, disease of the musculature, cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplantation, bowel ischaemia, pulmonary infarction, surgical occlusion of blood flow, soft tissue injury, skeletal muscle reperfusion injuries, glaucoma, macular degeneration of the eye, diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are used as catalytic scavengers of reactive oxygen species to protect against ischaemia reperfusion injuries associated with myocardial infarction, stroke, acute head trauma, organ reperfusion following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scavengers, where the metal is manganese, copper or iron. The porphines exhibit cardiant; cerebroprotective; vasotropic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's disease; neurological disorder; arthritis; hypertension; artherosclerosis; oedema; septic shock; pulmonary hypertension; asthma; impotence; infertility; endometriosis; diabetes; pneumonia; human; cystic fibrosis; sinusitis; autoimmune disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organ reperfusion; bowel ischaemia; pulmonary infarction; glaucoma; skeletal muscle reperfusion injury; central nervous system disease; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive; hypotensive; antidiabetic; antigout; antiasthmatic; and virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 24; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-664150/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                         with myopathies, neurological disorders, arthritis, systemic
                                                                                                                                                                                                                                               fatigue of congestive heart failure, muscle weakness syndrome associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity. The porphines act as superoxide dismutase (SOD) inhibitors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiparkinsonian; nootropic; anticonvulsant; cytostatic; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to porphines and their metal complex oxidant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalytic oxygen scavengers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New metal complexes of methine substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY94782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6127356-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  superoxide dismutase; myocardial infarction; stroke; acute head trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphine;
   EC-SOD gene. EC-SOD is a tetrameric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metal complex oxidant scavenger; inhibitor; EC-SOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fridovich I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
5139..5804
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/note= "Superoxide dismutase"
5085..5138
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glycosylated copper
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                                                                                                                                                Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the contains of the S. pneumoniae genome to primers derived from the fragment of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to prime the sequence of the S. pneumoniae genome to grant of the S. pneumoniae genome to genome the sequence the sequence of the S. pneumoniae genome to genome the sequenc
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           readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10079 BP; 2482 A; 2612 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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                                                                                                                            primers derived from the fragment of the S. pneumoniae g
the amplification and isolating the amplified sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 593-602; 1409pp; English
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Pred. No. 1.1e
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                                                                                                                                                                                                                                                                                                                                                                                                                               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DAA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                              specification, but was obtained at ftp.wipo.int/nub/nub/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000\ \mathrm{or} more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 32932; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 32932.
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                                                                                                                                                                                                                                                                                                          215 A; 205 C; 202 G; 122 T; 0 other;
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Pred. No. 1.1e+02;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 32911; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                Sequence 2510 BP; 680 A; 581 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000; 2000US-0614150
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                                                                                                                             Conservative
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Pred. No. 1.5e+02;
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9558 BP; 1853 A; 2675 C; 2996 G; 2034 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valencia orange ribosomal RNA gene - also probes and primers derived from citrus fruit rRNA gene spacer regions, useful for RFLP analysis of citrus fruit
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                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                               BAC containing repeats from centromeres 1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCGCTTCACTCGCCGTTACTA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                        2000WO-US07392
99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0227806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function= probe
/note= "claimed"
9397..9558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0227806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7338..8291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= 28s_rRNA 5583..9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= 18S_rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*taq=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ν̈́O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Search completed: October 17, 2002, 08:50:39

0;

Job time : 159.778 secs

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                                                                                                                         Db 45271 CCGGTTCGCCGCTTACTA 45251
                                                             Best Loc
Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                Claim 102; Page 351-364; 1449pp; English.
                                                                                                                                                                                                                                                                                          Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells \,\cdot\,
                                                                                                                                                   selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                 The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for
                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587529/55
                                                                                                                        Sequence 59590 BP; 17614 A; 12031 C; 13575 G; 16118 T; 252 other.
                                                                                                                                                                                  the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                  producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                                                                                        Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1999;
                                                                            Local
                              1 CCGCTTCACTCGCCGTTACTA 21
                                                             l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Copenhaver
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0154603
                                                                          80.9%;
                                                                                                                                                                                                                                                                                                                                                                                        Ó
                                                                                                                                                                                                                                                                                                                                                                                        Keith
                                                             0;
                                                                          Score 17.8;
Pred. No. 23
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        X
                                                                                            DΒ
                                                                                          21;
                                                               2;
                                                                                          Length 59590;
                                                               Indels
                                                               0;
                                                               Gaps
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2
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                                                                                                                                                                                                                                       AAV72868/c
                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            transcription termination and polyademylation region which preferably is active in plant cells. The present sequence represents an oligonucleotide from the present invention. Transformed plant cells and transgenic plants comprising the DNA constructs are used to produce a desired protein at a high yield, e.g. antibodies, insecticidal proteins (e.g. a Bt toxin), a protein useful in the food industry. Alternatively the constructs can be used to produce an antisense RNA or ribozyme. The use of intergenic ribozomal DNA enhances stability and the copy number or expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA construct has been developed which comprises the following operably linked DNA fragments: (a) a ribosomal DNA sequence, preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana; rRNA gene; ribosomal DNA; intergenic region; DNA-construct; plant; multiple Sall repeat; stability; copy number; transgene; antibody; insecticidal protein; Bt toxin; ss.
          19-MAY-1998;
                                   26-NOV-1998
                                                                                   Neospora caninum
                                                                                                                                                 Neospora caninum large subunit ribosomal DNA
                                                                                                                                                                           29-MAR-1999
                                                                                                                                                                                                   AAV72868;
                                                                                                                                                                                                                           AAV72868 standard; DNA; 3499
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    transgenes in a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived from a plant; (b) an expressible (especially plant-expressible) promoter region; (c) a heterologous coding region; and (d) a transcription termination and polyadenylation region which preferably i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 11; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA construct containing plant intergenic ribosomal DNA fragment containing multiple SalI repeats; increases stability and copy number of a transgene(s) in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bachmair A, Schweizer D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09813505-A1
                                                                                                                         Large subunit ribosomal DNA;
                                                                                                                                                                                                                                                                                        2 CCGGTTCGCTCGCCGTTACTA 22
                                                                                                                                                                                                                                                                                                                  1 CCGCTTCACTCGCCGTTACTA 21
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                           24 BP; 3 A; 9 C; 6 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                       (first entry)
           98WO-AU00367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96AT-0001695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-EP05217
                                                                                 (NC-Liverpool strain)
                                                                                                                                                                                                                                                                                                                                                      80.9%;
90.5%;
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                         LSU-rDNA; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  Score 17.8;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         0;
Вp
                                                                                                                                                                                                                                                                                                                                                   AAQ88228/c
                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
         misc_RNA
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livestock. It is recognised as being closely related to Toxoplasma gondi. Comparison of LSU rDNA of N. caninum with a consensus sequence derived for the LSU rDNA of T. gondii demonstrated that the 12 domain (C1/C1') region can serve as a target for the development of a species-specific PCR (see AAVT2869-75) for the
                                                                                                   detection of Neospora rDNA, especially in clinical samples. In addition, PCR MIMICS have been developed for use in competitive PCK assays (see AAV/23676-81) to differentially diagnose between Neosporaspp. and other related/non-related micro-organisms, particularly
                                                                                                                                                                                                                                                                                         fragments obtained by PCR amplification of N. caninum (NC-Liverpool strain) tachyzoite genomic DNA. N. caninum is a cyst-forming corcidian parasite that causes neuromuscular disease in canines and is a significant cause of abortion and meonatal mortality in
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large subunit ribosomal DNA of Neospora species, especially N. canhium - useful to derive nucleic acid sequences for isolation of Neospora species by PCR amplification, e.g. to diagnose Neospora ir clinical samples
                                         Sequence 3499 BP; 870 A; 734 C;
                                                                                                                                                                                                                                                                                                                                                                              This nucleotide sequence encodes the large subunit (LSU) ribosomal DNA (rDNA) of Neospora caninum. It is a compilation of overlappin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-045313/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amoyal GG, Ellis JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSE-) INSEARCH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1997;
                                                                                  Coxoplasma spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97AU-0006903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice
Score 17.8;
                                           937
                                           G; 958 T; 0 other;
  DB 20;
    Length 3499;
                                                                                                                                                                                                                                                                                                                                                                                overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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misc_RNA
                                                                                           misc_RNA
                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                          Citrus sp
                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                                     DNA fingerprinting; restriction fragment length polymorphism; ds
                                                                                                                                                                                                                                                                                      Ribosomal RNA; rRNA; 18S; 28S; 5.8S; Valencia orange; RFLP analysis;
                                                                                                                                                                                                                                                                                                                      Valencia orange ribosomal RNA gene.
                                                                                                                                                                                                                                                                                                                                                         24-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                       AAQ88228;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ88228 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                           /product= 5.8S_rRNA
2012..2238
/function= spacer
2239..5582
                                                                                                                                           /product= 185_rRNA
1598..1848
                                /*tag=
                                                                                            1849..2011
                                                                                                           /function= spacer
                                                                                                                           /*tag=
                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                             /*tag=
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AAV36211/c
                                                                                                                         RESULT 11
AAV83003/c
  XX DX DX XX
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                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                Pheumocystis carinii in immunosuppressed Sprague-Dawley rats. The specification describes a method for the diagnosis of Pheumocystis carinii which comprises detecting the presence of a nucleic acid sequence containing the 26S rRNA gene specific for P. carinii in a sample. The 26S rRNA gene in a sample is amplified, and the primer extension products detected by hybridisation with a labelled cligonucleotide. The methods can be used for the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of Pneumocystis carinii - by amplification of nucleic acid from sample with PCR primers specific for the 26S rRNA gene of Pneumocystis carinii
                             Contiguous sequence determined for P. carinii from immunosuppressed rats
                                                                                    AAV83003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-398016/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11S5776680-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection; diagnosis; 26S rRNA gene; P. carinii specific; infection; species identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total contiguous sequence of P. carinii in immunosuppressed rats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV36211;
                                                                                                               AAV83003 standard; DNA; 4256 BP
                                                                                                                                                                                                                                                                                              Sequence 4256 BP; 1190 A; 766 C; 1124 G; 1176 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       P. carinii infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the total contiquous sequence of Pneumocystis carinii in immunosuppressed Sprague-Dawley rats. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Columns 29-34; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leibowitz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV36211 standard; DNA;
PCR amplification; sequencing; assay; inhibitor; nuclear rRNA gene;
                                                       23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1995;
                                                                                                                                                                                   660 CCACTTCACTCGCCGTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
                                                                                                                                                                                                                                        Local Similarity
wes 19; Conserv
                                                                                                                                                                                                            1 CCGCTTCACTCGCCGTTACT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTTCACTCGCCGCTACT
                                                                                                                                                                                                                                         Conservative
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0922987
94US-0298087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0505509
                                                                                                                                                                                                                                                   83.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4256 BP
                                                                                                                                                                                                                                                                                                                                       for the detection of various species of
                                                                                                                                                                                   641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                   Score 18.4; DF
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                        ----
                                                                                                                                                                                                                                                                  Length 4256;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                        0;
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AAV31383
ID AAV3
XX
AC AAV3
XX
DT 07-9
DE 0119

AAV31383;

AAV31383 standard; DNA;

24

ВΡ

07-SEP-1998

(first entry)

Oligonucleotide Q SEQ ID NO:5 from W09813505

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dC
                                                   QУ
RESULT 12
                                                                                   Query Match
Best Local :
                                                                          Matches
                                                                                                                                               The present sequence represents the contiguous sequence determined for Pneumocystis carinii from immunosuppressed Sprague-Dawley rats, using the in vitro method of the invention. The method assays for an inhibitor of the catalytic Group I self-splicing intron reaction in the nuclear rRNA genes of P. carinii. The method is useful for screening potential drugs for treating P. carinii infections before more costly animal
                                                                                                                                                                                                                                             Screening assays for drugs against Pneumocystis carinii - based inhibition of 26S rRNA gene intron self-splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Кеу
                                                                                                                                                                                                                                                                              WPI; 1999-069716/06.
                                                                                                                                                                                                                                                                                                                                             30-JUL-1992;
19-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pneumocystis carinii.
                                                                                                                 Sequence 4256
                                                                                                                                                                                                                         Example 1; Fig 2; 51pp; English.
                                                                                                                                                                                                                                                                                                                         (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY
                                                                                                                                                                                                                                                                                                                                                                  27-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                  US5849484-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catalytic Group I self-splicing intron reaction; drug screening; ss.
                                                                                                                                        testing
                                                                                                                                                                                                                                                                                                   Leibowitz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                               660 CCACTTCACTCGCCGTTACT 641
                                                    1 CCGCTTCACTCGCCGTTACT
                                                                          19;
                                                                                   Similarity
                                                                                                                                        is conducted
                                                                          Conservative
                                                                                                                  BP; 1190 A; 766 C; 1124 G; 1176 T; 0 other
                                                                                                                                                                                                                                                                                                   Liu Y;
                                                                                                                                                                                                                                                                                                                                            93US-0068248.
92US-0922987.
95US-0491690.
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217..374
                                                                                                                                                                                                                                                                                                                                                                                      95US-0491690
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/note= "5.8S
375..556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "internal transcribed spacer
557..4256
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= f
/note= "26S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                  83.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
"3'-terminal portion of intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                    20
                                                                          0;
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                                                                                   Score 18.4; D
Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 16SrRNA"
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcribed
                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spacer
                                                                                             20;
                                                                                             Length 4256;
                                                                          Indels
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RESULT 8
AAZ57868
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           It is characterised as an RNA binding protein (RNP-1). The invention provides PRGE polypeptides (see AAY58608-38) and polynucleotides (see AAZ57839-69), expression vectors, host cells, antibodies, agonists and antagonists. It also provides methods for diagnosing, treating or preventing disorders associated with expression of PRGE. Polynucleotides are also used as sources of probes and primers for diagnosis and monitoring of disease, also for detecting related
                                                                                                                                       PANCTUTO2, and the full-length sequence assembled from overlapping clones from a number of libraries. PRGE-30 is expressed in nervous
                                                                                                                                                                  The present sequence is that of Incyte clone 1977214 encoding new human protein regulating gene expression PRGE-30 (see AAY58637). cDNA was initially isolated from pancreatic tumour cDNA library
                                                                                                                                                                                                                                                   New human polypeptides that regulate gene expression, prevention and diagnosis of, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein regulating gene expression; PRGE-30; human; cell proliferation; antiproliferative; inflammation;
                                                                                                                                                                                                                       Claim 9; Page 146-147; 150pp; English
                                                                                                                                                                                                                                                                                                         WPI; 2000-116543/10.
                                                                                                                                                                                                                                                                                                                                     Guegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ57868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ57868 standard; cDNA; 3073 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2780 CCGCTTCACTCGCCGCTACT 2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3040 BP; 851 A; 686 C; 976 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma, ductal carcinoma in situ or lobular carcinoma in situ. This
                                                                                                                         reproductive and gastrointestinal tissues associated with cell
                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09964596-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antlinflammatory; gene therapy; diagnosis; RNA binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein regulating gene expression PRGE-30 cDNA cione 1977214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents DNA encoding a human HET polypeptide
                                                                                                           proliferation and inflammation diseases, disorders or conditions
                                                                                                                                                                                                                                                                                                                                                     Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                          14-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               il Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                        Yue H, ic.
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in gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0089029
98US-0094575
                                                                                                                                                                                                                                                                                                                                                                                                         98US-0104624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 122..2875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%;
                                                                                                                                                                                                                                                                                                                                     ΥT,
                                                                                                                                                                                                                                                                                                                                     Hillman JL,
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                    Bandman O,
                                                                                                                                                                                                                                                                                                                                      Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527
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                                                                                                                                                                                                                                                                                                                                     Corley NC;
                                                                                                                                                                                                                                                                  for treatment,
                                                                                                                                       in nervous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3040
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1 CCGCTTCACTCGCCGTTACT

Query Match
Best Local Similarity
Matches 19; Conserv

Conservative

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Mismatches

ب

Indels Length

0 Gaps

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Score 18.4;

DB 22;

3130;

Sequence 3130

B₽:

566 A; 1005 C; 83.6%; 95.0%;

703 G; 856 T; 0 other;

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Qγ
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AAI92675/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2854 CCGCTTCACTCGCCGCTACT 2873
                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemla, inflammation and immundiagnosing and treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI92675 standard; cDNA; 3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3073 BP;
                           at ftp.wipo.int/pub/published_pct_sequences
                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                  activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                  production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                            The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 12735; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                                                 Tanq YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; peptide therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 12735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI92675;
                                                                                       treatment of cancer, leukaemia, nervous system
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAO12744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue growth
                                                                          inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCGCTTCACTCGCCGTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disorders;
                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor; immunomodulatory; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699 C;
                                                                                                                                                                                                                                                                                                                                                                                                 RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                         disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3073;
                                                                                         arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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This invention describes a nucleic acid seqment that encodes a novel human HET polypeptide which has cytostatic activity. The HET protein binds to the hsp27 promoter in order to suppress expression of the hsp27 protein. The HET protein (Hsp27-ERB-TAT binding protein) can bind to the hsp27 promoter and suppress expression of hsp27. The HET acts as tumour suppressor gene. The products and methods can be used for the diagnosis and prognosis of breast cancers including infiltrating duct carcinoma, lobular carcinoma, medullary carcinoma, mucinous carcinoma, tubular carcinoma, ductal carcinoma in situ and lobular carcinoma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                HET; cytostatic; hsp27 promoter; suppressor; hsp27; tumour suppressor; Hsp27-ERE:TAT binding protein; diagnosis; prognosis; breast cancer; infiltrating duct carcinoma; lobular carcinoma; medullary carcinoma; mucinous carcinoma; tubular carcinoma; ductal carcinoma; therapy;
                                                                                                                                       Claim
                                                                                                                                                                                                                                  Osborne CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HET cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX78193 standard; cDNA; 3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 19; 35pp; Japanese
                                                                                                                                                                New isolated tumor suppressor, HET
                                                                                                                                                                                                                                                Allred CD,
                                                                                                                                                                                                                                                                          (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                      04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                   WO9928466-A1
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 899 BP; 233 A; 200 C; 224 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maintaining accuracy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragments were generated by an EcoRI digest. This is used as a probe for detection of Candida infection. The advantage of this probe is that diagnosis time can be reduced from 3-4 days to 1-2, while
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic DNA was isolated
                                                                                                                                                                                                                                                                                                                               30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe for detection of infectious disease - fragment specific for fungal disease agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-167493/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       757
                                                                                                                                                                                            ·PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                           1999-385382/32
)B: AAY08991.
                                                                                                                                     3; Page 126-127; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                             Fuqua SAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                    97US-0068132
                                                                                                                                                                                                                                                                                                                               98W0-US25381
                                                                                                                                                                                                                                                                                                                                                                                                                                       ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.6%;
95.0%;
                                                                                                                                                                                                                                                Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Candida albicans
                                                                                                                                                                                                                                                AV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 8
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                                                                                                                                                                                                                                               O'Connell P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                             Desterreich S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CA-26) (AAQ63962)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                   nuclear matrix protein, HET, (also known as scaffold attachment factor B or SAF3) to form a complex and measuring the amount of HET polygeptide present. A decrease in HET level in the sample compared to the control indicates a presence of antioestrogen resistance. Resistance in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2780
            resistance in breast cancer cells, as well as a decrease in chance of survival. The cancerous cells may be from an infiltrating duct carcinoma
                                         diagnosed by determining loss of heterozygosity (LOH) at a chrolonus where the LOH at the locus is indicative of antioestrogen
                                                                                      cancer cells can be predicted by comparing the amount of samples from patients with antioestrogen-resistant and
                                                                                                                                                                            breast cancer cells, comprising obtaining a breast cancer cell sample, contacting the sample with an antibody that specifically binds to the
                                                                                                                                                                                                                                                                  Detection of antioestrogens breast cancer cells comprises measurement of a HET polypeptide - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HET; nuclear matrix protein; antioestrogen resistance; breast cancer; scaffold attachment factor B; SAF-B; loss of heterozygosity; human; hinfiltrating duct carcinoma; lobular carcinoma; medullary carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          situ. The products can also be used for therapy and in the screening of compounds for activity in either stimulating HET activity, overcoming the lack of HET or blocking the effect of a mutant HET molecule.
                                                                     antioestrogen-sensitive breast cancers. Malignant breast cancers can
                                                                                                                                                                                                        The invention relates to the detection of resistance to anticestrogens
                                                                                                                                                                                                                                      Examples; Page 137; 140pp; English.
                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                              Oesterreich S, Osborne CK,
                                                                                                                                                                                                                                                                                                                                                                                            (TEXA ) UNIV TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mucinous carcinoma; tubular carcinoma; ductal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HET DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS12099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS12099 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCGCTTCACTCGCCGTTACT
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                                                                                                                                                                                                                                                                                                                                  2001-536660/59.
                                                                                                                                                                                                                                                                                                                   AAU07605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3040 BP; 851 A; 686 C; 976 G; 527 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19p13.2-p13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US06135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 54..2801 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                              SA
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                                                          a chromosome!
                                                                                                     HET protein in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOLL;
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carcinoma, medullary carcinoma, mucinous

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AAQ39050/c
ID AAQ39050 standard; DNA; 6824 BP.
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Best Local S
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11-DEC-1991;
24-NOV-1986;
07-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides novel methods of producing probes for use in the identification of a number of microorganisms. These include E. coli, Mycobacteria, Mycoplasma, Campylobacter, Chiamydia, Enterobacter, Legionella, Salmonella, Pseudomonas, Neisseria gonorrheae, fungi and
                                                                  Vector for Kluyeromyces lactis and Saccharomyces cerevisiae which allows stable multiple integration of DNA for prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae; E. coli; domain; yeast; plasmid; promoter; expression cassette; HIS3; marker; transformant; human; lysozyme; HLZ; GAL7; signal sequence; killer toxin; transcription termination signal;
                   Claim
                                                    heterologous proteins
                                                                                                                             WPI; 1993-127394/16
                                                                                                                                                                  Galeotti CL,
                                                                                                                                                                                                     (ISTS ) SCLAVO SPA.
                                                                                                                                                                                                                                            04-SEP-1991;
                                                                                                                                                                                                                                                                                                                     21-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic; vector; integration; Kluyeromyces lactis; 255 ribosomal DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.lactis/S. cerevisae genetic vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3550 BP; 941 A; 697 C; 1000 G; 912 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-viral non-target species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing a probe for nucleic acid hybridization assays comprises constructing a nucleotide polymer sufficiently complementary to hybridize to an rRNA region that distinguishes non-viral target from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                31-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                  FLP; 2 micron plasmid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McDonough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 CCGCTTCACTCGCCGTTACTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCGCTTCACTCGCCGTTACTA 21 \mathcal U
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             1; Fig 1; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                Gallo E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kop JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87WO-US03009.
91US-0806929.
86US-0934244.
87US-0083542.
                                                                                                                                                                                                                                          91IT-0MI2349
                                                                                                                                                                                                                                                                                92EP-0114838
                                                                                                                                                                  Riccio ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hogan JJ;
                                                                                                                                                                Rossolini GM,
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0.45;
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                                                                                                                                                                  Thaller MC;
                                                                      of
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A CONTRACTOR OF THE PROPERTY O
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AAQ63962/c
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                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                       23-OCT-1992;
                                                                                                                                            25-OCT-1993;
                                                                                                                                                                                                                       W09410341-A.
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CC inbosomal DNA from S. cerevisiae, flanking a genetic marker suitable CC for selection of the yeast transformants in which the integration CC event has occured. Other DNA sequences may be introduced into the CC integration plasmid, such as expression cassettes. The gene HIS3 CC from K. lactis and S. cerevisiae is pref. used as a genetic marker CC for the selection of transformants and an expression cassette for the CC production and secretion into the culture medium of human lysozyme. CC This complete transformation vector is 7850 bp long and includes the CC integration vector of the invention and an expression cassette CC comprising the K. lactis GAL7 promoter, the signal sequence of the K. CC lactis killer toxin, the cDNA encoding the ripe form of human lysozyme CC (HLZ) and the transcription termination signal FLP of the 2 micron CC plasmid from S. cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                integrating vector which comprises a region necessary for the stable maintenance of the plasmid in E. coli and a domain which acts as an integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting of two not contiguous sequences of the 20 integrating unit consisting unit consisti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of infectious disease; fungal disease agent; probes; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans (CA-26) genomic DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ63962 standard; DNA;
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(FUSO ) FUSO PHARM IND LTD
                                                       (FUSO ) FUSO YAKUHIN KOGYO KK.
(ONOY/) ONO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 CCGCTTCACTCGCCGTTACTA 124
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                                                                                                                                                                                                                   92JP-0285802
                                                                                                                                                                                                                                                                                                                             93WO-JP01555
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/note= "fragment isolated and
for probe formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517..737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "fragment isolated and for probe formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "fragment isolated and for probe formation"
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Hirotsu T,

Keshi H, Matsuhisa A,

Ohno

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid, or polypeptides encoded by the nucleic acids, can be used to identify compounds that inhibit or activate a polypeptide involved in induced resistance, by contacting the cell or polypeptide with one or more test compounds and identifying compound(s) that specifically modulate the activity of the polypeptide. Plant protection agents can be prepared by formulating the identified compounds in a form suitable for their uptake and optionally metabolization in organisms, especially plants, phytopathogenic fungi, nemalization in organisms, especially plants, phytopathogenic fungi, nemalization in sect pests. The nucleic acids or regulatory regions, or corresponding vectors, or the polypeptides encoded by the nucleic acids, or compounds identified as
                                                                                                                                                                                                                                                           expressed sequence tag: Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides encoded by the nucleic acids, or compounds identified as above, can be used to improve the pathogen resistance of plants or to produce transgenic plants. The nucleic acids or regulatory regions, or vectors, cells, plants or plant tissues containing them, or the polypeptides and antibodies to the polypeptides, can be used to screen for new plant protection agents or genes involved in induction of resistance in plants. Vectors containing the nucleic acids, or the
                                         22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                  Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                         Fusarium venenatum EST SEQ ID NO. 2091.
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF09568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF09568 standard; cDNA; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 218 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory regions or recombinant DNA molecule or vectors containing them, or the compounds identified as above, or the polypeptides or antibodies, can be used in diagnostic compositions. AR238676-Z33888 represent fragments of tobacco cDNA which are associated with plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identifying a compound or sample that suppresses or activates and/or enhances expression of the marker. Host cells containing the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used to identify compounds useful for plant protection by transforming a cell with a recombinant DNA molecule containing a selectable and/or detectable marker linked to the regulatory region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel cDNA molecules corresponding to tobacco (Nicotiana tabacum) genes that are expressed in response to tobacco mosaic virus (TMV) infection. Regulatory regions that provide specific
(NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                28-SEP-2000
                                                                                                                                                                           WO200056762-A2
                                                                                                                                                                                                                  Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1a; 49; 130pp; German.
                                                                                22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of the nucleic acids
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                                         99US-0273623
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100.0%; Pred. No. 0.11;
tive 0; Mismatches
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AAF23019/c ID AAF23(

AAF23019 standard; rRNA;

3550

20-MAR-2001 (first entry)

Yeast 28S rRNA sequence

AAF23019;

RESULT 3

B 80

Matches Query Match Best Local

Similarity

100.0%; 100.

Score 22; Pred. No.

Conservative

0;

Mismatches

Indels

0;

Gaps

0;

0.12;

DB 21; Length 431; 0;

Sequence 431 BP; 139 A; 78 C;

115 G; 96 T; 3 other;

PRRY PROSE

bacterium;

Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA; Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella; Salmonella; Pseudomonas; Campylobacter; Nelsseria gonorrheae; fungus;

22-FEB-1994; 24-NOV-1987;

94US-0200866 87US-0295208 95US-0454063

30-MAY-1995;

US6150517-A

Saccharomyces cerevisiae

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engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Asperqillus niger; AAF11854 to AAF11858 represents ESTs from Asperqillus oryzae; and AAF11859 to AAF1387 represents ESTs from Asperqillus oryzae; and AAF18679 to AAF1337 represents ESTs from Triboderma reesei, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from Fr cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells amont to changes in culture conditions, environmental stress, spore more to the conditions of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 86; Page 1160; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                  all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           morphogenesis, recombination, metabolic or catabolic pathway
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ALIGNMENTS

Tobacco; plant; resistance; tobacco mosaic virus; TMV; infection; protection; plant protection agent; phytopathogenic fungi; nematode; insect pest; pathogen resistance; transgenic plant; diagnosis; ss. AAZ33745 standard; cDNA; 218 BP WPI; 1999-552163/47 Nicotiana tabacum. Tobacco plant resistance-associated cDNA fragment 70. 09-DEC-1999 (first entry) Schreier P, (FARB) BAYER AG 25-MAR-1998; 25-MAR-1998; 30-SEP-1999 DE19813048-A1. Garbers C, 98DE-1013048 98DE-1013048 Langen G, Kiedrowski

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Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-378-313-18
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US-08-778-912A-1
US-09-541-941B-1
US-09-541-941B-1
US-09-541-941B-2
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ALIGNMENTS

: Sequence 1013, Application US/08998416 : Patent No. 6239264 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: MOLECULE TYPE: ORIGINAL SOURCE: TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587 TELEFAX: 919-541-8689 FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Mohr, Christine SEQUENCE CHARACTERISTICS: LENGTH: 666 base pairs TYPE: nucleic acid NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA ORGANISM: PAG1621UP STRANDEDNESS: single APPLICATION NUMBER: FILING DATE: 24-DEC Wendland, Jurgen Knechtle, Philipp linear No. DNA (genomic) 24-DEC-1997 6239264artis Corporation CH 0016/97 1152 US/08/998,416 Peter PF/5-30306/A/CGC1976

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Query Match
Best Local Similarity
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                                                                                                                             Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                            MOLECULE TYPE: ORIGINAL SOURCE:
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LENGTH: 697 base pairs
TYPE: nucleic acid
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TELEPHONE: 919-541-8587
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APPLICATION NUMBER: CD 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                           332 CCGCTTCACTCGCCGTTACTA 352
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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Research Triangle Park
No. 6239264th Carolina
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Steiner, Sabine
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Knechtle, Philipp
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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24-DEC-1997
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                                                                                                                         95.5%; Score 21; DB 4; Length 697; 100.0%; Pred. No. 0.057;
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Best Local Similarity 100.0%;
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                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
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LENGTH: 699 base pairs
TYPE: nucleic acid
companyments: 620
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                        APPLICANT:
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TELEPHONE: 919-541-8587
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APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Research Triangle Park
: No. 6239264th Carolina
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Pohlmann, Rainer
Steiner, Sabine
                                    Wendland, Jurgen
Knechtle, Philipp
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Knechtle, Philipp
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Mohr, Christine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                      95.5%; Score 21; DB 4; Length 699; 100.0%; Pred. No. 0.057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38,241
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                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                    APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
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                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 CCGCTTCACTCGCCGTTACTA 352
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             COUNTRY: U
ZIP: 27709
                                                                                         ADDRESSEE: No. 6239264artis Co
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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TELEFAX: 919-541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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No. 6239264th Carolina
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                                                                            USA
                                                                                                                                                                                                                                                          Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                  Mohr, Christine
                                                                                                                                                                                                                                                                                                               Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                      Philippsen, Peter
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                                                                                                                                               No. 6239264artis Corporation
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GENERAL INFORMATION:
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: (
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA 4-285802
FILING DATE: 23-OCT-1992
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,831B
NAME: GASS, David A.
REGISTRATION NUMBER: 38,153
REFERENCE, DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                FILING DATE: 19-JUN-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ohno, Tsuneya
APPLICANT: Hirotsu, Takuo
APPLICANT: Keshi, Hiroyuki
APPLICANT: Matsuhisa, Akio
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                                                                          FILING DATE: 23-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
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                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 St
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 CCGCTTCACTCGCCGTTACTA 352
                                                                                                                                                         APPLICATION NUMBER: PCT/JP93/01555 FILING DATE: 25-OCT-1993
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe for Diagnosing Infectious Diseases
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                    19036/32578
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US-08-505-509-31
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                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/08505509 Patent No. 5776680
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 899 base pairs
                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4256 base pairs
TYPE: nucleic acid
                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                         FILING DATE: 30-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liebowitz, Michael J. APPLICANT: Liu, Yong
                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                            TOPOLOGY:
                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                              REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UND1-009
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STRAIN: Clinical Isolate CA-26
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                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Princeton
                                                                                                                                                                                                                                                NAME:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Richard R. Muccino STREET: P.O. Box 1267
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                                                                                                                                                                                                                                              Muccino, Richard R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                (609) 466-3407
(09) 466-2760
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                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
83.6%;
95.0%;
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95.0%;
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Score 18.4; D
Pred. No. 1.4;
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Pred. No. 1.2;
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           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 899;
           Length 4256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                     ; Sequence 18, Application US/08378313
; Patent No. 6207881
                                                                                                                                                                                                                                                                                                                                                                            US-08-491-690A-31
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Patent No.
                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (908) 273-4679
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
              APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leibowitz, Michael J.

APPLICANT: Liu, Yong
TITLE OF INVENTION: In Vitro Assay For Inhibitors
TITLE OF INVENTION: Of The Intron Self-Splicing Reaction in Pneumocystis Carini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,538
REFERENCE/COCKET NUMBER: UMD1-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 273-4988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07901
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       660 CCACTTCACTCGCCGTTACT 641
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OPERATING SYSTEM:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Summit
STATE: New Jersey
                                                                                                                                                                                                                                                                                                          Local Similarity
nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/491,690A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                       1 CCGCTTCACTCGCCGTTACT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                            4: 4256 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muccino, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      758 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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95.0%;
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Pred. No. 1.4;
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RESULT 10
US-08-378-313-20
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Patent No. 6207881
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA: US 07/862,493
                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THEOLOGIS, ATH APPLICANT: SATO, TAKAHIDO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                  FILING DATE:
                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CGCTTCACTCGCCGTTACTA 21
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California
                                                                                                                                                                                                                      California
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                                                                                                                                                                                                                                                                                                                                                                             THEOLOGIS, ATHANASIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                      MORRISON & FOERSTER
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90.0%;
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                                                                US/08/378,313
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Pred. No. 8.1;
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-308-461-3
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US-08-308-461-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Jeffrey W. Voss

APPLICANT: Connie Caron

TITLE OF INVENTION: Inducers of Gamma Globin Gene Expression

TITLE OF INVENTION: and Screening Assays Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08308461
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                                                                                                                          TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                          REFERENCE/DOCKET NUMBER: BB TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 22-7400
                                                                                                                                                                                                                            FILING DATE: 16-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4872 CGCCTCACTCGCCGTTAGTA 4891
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ATTORNEY/AGENT INFORMATION:
                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TELEFAX: (%)
TELEFAX: (%)
TELEFAX: (%)
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                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
                                                 STRANDEDNESS: single
                                                                                                                                                                                                               REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/308,461
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFHONE: (415) 856-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                        CENGTH:
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                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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                                                                                    33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                   linear
                oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                BB1-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; D
Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 9060;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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0;

Score 16;

DB 1;

Length 33;

CORRESPONDENCE ADDRESS:

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RESULT 13
US-09-106-464-1/c
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                                                                                                                                                                                                                                                                                                                                                              °CT-US95-11823-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                            Sequence 1, Application US/09106464 Patent No. 6011145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9511823 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                           GENERAL INFORMATION:
                                             APPLICANT: Steffens, John C. APPLICANT: Ghangas, Gurdev S. APPLICANT: Kuai, Jian-Ping APPLICANT: Eannette, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Inducers of Gamma Globin Gene Expression TITLE OF INVENTION: and Screening Assays Therefor
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            Local Similarity hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 33 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/11823 FILING DATE:
                                                                                                                                                                                                                              1 TICACTCGCCGTTACT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                           5 TTCACTCGCCGTTACT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 State Street, Suite 510
                                         Eannetta, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                          72.7%;
Chain Length Specific UDP-Glc:Fatty Acid Glucosyltranferases : 2
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US-08-778-912A-9
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; Patent No. 5876977
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wang, Jun
APPLICANT: Ngan, F N
APPLICANT: But, P P
APPLICANT: Shaw, P C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Spector, Eric S.
REGISTRATION NUMBER: 22495
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
       COMPUTER READABLE FORM:

MEDIIM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERAVING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    APPLICANT: Shaw, P C
TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT
TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
TITLE OF INVENTION: TRADITIONAL CHINESE MEDCINES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1291 CTTCACTCGCCATTACT 1275
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER:
                                                                                                                                                                                   CITY:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Bo. CITY: Arlington
                                                                                                                                             COUNTRY:
                                                                                                                                                                    STATE:
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/106,464
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                                                                                                                                                              New York
                                                                                                                                10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Jones, Tullar & Cooper, P.C.
P.O. Box 2266 Eads Station
                                                                                                                                                                                                 E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1627 base pairs
                                                                                                                                               USA
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94.1%;
US/08/778,912A
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Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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; MOLECULE TYPE: US-08-778-912A-11
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US-08-778-912A-11
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                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEPHONE: 212 391 0526
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Chap, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 5218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEFAX: 212 391 0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08778912A Patent No. 5876977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.2%; Score 15; DB 2; Best Local Similarity 100.0%; Pred. No. 41; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Jun
APPLICANT: Ngan, F N
APPLICANT: Ngan, F N
APPLICANT: Shaw, P C
TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
TITLE OF INVENTION: TRADITIONAL CHINESE MEDCINES
RUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                            LENGTH: 20 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                        DNA (genomic)
  68.2%; Score 15;
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BER: 52188
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DB 2;
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Length 20;
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTCGCCCTTACTAG 22
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Search completed: October 17, 2002, 08:51:48 Job time: 33.2889 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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     11111111
7654321098765432
                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                          Score
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                                                                                                                                                                                                                                                                                                                                                                                                                               seq
    derived
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length: 2000000000
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Match Length
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100.0
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95.5
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95.5
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Gapop 10.0 , Gapext 1.0
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22
                                                                                                                                                                                                                                                              10:
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Compugen Ltd
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AW724745 f7hl0nm.f
AI320035 B8902mm.f
AI320035 B8902mm.f
BE:77149 MY-11-E-0
AI904502 PM-BT057-
AW981798 PC18H03 P
AW982734 PC23A10 P
AW982734 PC23A10 P
AW754445 PC03D12 P
BE356832 DG1_145_D
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A2927057 4911.fd63
AZ923337 474.dhz98
AZ933397 474.dhz98
AZ932397 474.dhz98
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ALIGNMENTS

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=PM&t2=PM-BT057-305.html
&t3=20199&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers Simpson, A.J.

Shotqun sequencing of the human transcriptome with ORF sequence tags

sequence tags Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., ('Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and A.1904941 309 bp mRNA linear EST 30 PM-BT057-290199-305 BT057 Homo sapiens cDNA, mRNA sequence .1904941 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 309) AI904541.1 GI:6494928 Tel: +55-11-2704922 Fax: +55-11-2707001 Homo sapiens Contact: Simpson A.J.G. Natl. Acad. Sci. U.S.A. /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BT057" 309 bp 97 (7), 3491-3496 (2000) 01509-010, Sao Paulo-SP, EST 30-MAR-2000 expressed

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RESULT 2
AW724745
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158 CCGCTTCACTCGCCGTTACTAG 179
                                                                           Local Similarity hes 22; Conser
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hes 22; Conserv
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Two Neurospora crassa EST Databases
Unpublished (1998)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW724745 311 bp mRNA linear EST 19-AF f7h10nm.f1 Neurospora crassa morning cDNA library Neurospora cDNA clone f7h10nm 5', mRNA sequence.

AW724745 GI:7619305
                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: Universal Forward Primer High quality sequence stop: 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      We anticipate the future release of the cDNA clones Genetics Stock Center \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: broe@ou.edu
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/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.
716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
87 a 67 c 90 g 65 t
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                                                                                                                                                                                                                                                                                                                                  /organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
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end of cDNA cloned into XbaI site of pBluescript; 3'
d of cDNA cloned into EcoRI site of pBluescript"
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                                                                                     Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F. Initial assessment of gene diversity for the comycete pathogen Phytophthora infestans based on expressed sequences Fungal Genet. Biol. 28 (2), 94-106 (1999) 20056376
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  Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen,
                          Wageningen University
                                                                                                                                                                                                                                                     Phytophthora infestans
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22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Bruce A. Roe, University of Oklahoma, broe@on.edu bepartment of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklaho 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "14,H., Lai,H., Kupfer,D., Dunlap,J
Two Neurospora crassa EST Databases
Unpublished (1998)
                                                                      Contact: Govers F
                                                                                                                                                                                                              Phytophthora
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We anticipate the future release of the cDNA clones to the Fundal
Genetics Stock Center
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/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="b8g02mm"
/clone_lib="Neurospora crassa morning cDNA library"
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/strain="mppR7602, Ai mating type"
/db_xref="taxon:4787"
/clone_lib="pinfestansMY"
/clone_lib="ai-week old vegetative, non-sporulating
/dev_strain="taxon:4787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G. etics
Contact: Simpson Cancer Genetics
Laboratory of Cancer Geneer Research
Ludwig Institute for Cancer 109, 4 andar, 01509-010, Sao Paulo-SP,
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                      Email: asimpsoneludwig.org.br the FAPBSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL project. This entry can be seen in the following the project. This entry can be seen in the following the project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=pM&t2=pM-BT057-347.html the project. This project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=pM&t2=pM-BT057-347.html for the following URL (http://w
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             /clone_lib="BT057"
                                                                                             /organism="Homo sapiens"
                                                              /db_xref="taxon:9606"
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pred. No. 2.2;
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Contact: Ross Whetten
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Tel: 919-515-7800
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Rorest Biotechnology Group
Dept. Of Forest Elate University
The Carolina State University
The Carolina State University
The Carolina State University
The Carolina State University, 6113 Jordan Hall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 CCGCTTCACTCGCCGTTACTAG 82
                                                                                                                                       The Pine Gene Discovery Project
Contact: Ross Whetten
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Pinus taeda
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/dev.stage="immature"
/note-stage="immature"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rosswhet@unity.ncsu.edu
Seq primer: 5, lambda TriplEx2 Sequencing Primer.
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PC23A10 Pine Triplex pollen cone library pinus taeda cDNA clone
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100.0%; Su
100.0%; Pre
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/clone="pc23410"
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                                                  Email: Imprateuga edu
Sequences have been trimmed to exclude PolyA, vector and regions
'~ 20 Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                     Department of Botany
The University of Georgia
The Triant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cordonnier Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bloolor
Eukaryota, Viildiplantae, Streptophyta, Embryophyta, Magnoliophyta, Lillopsida, Poales, Tracheophyta, (bases 1 to 517)

Common Common
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DG1_145_D09.b1_A002 Dark Srown l (DG1) Sorghum bicolor cDNA, meNA
                         Location/Qualifiers
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       /db xr. "Sora...
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/dev_Stage="immature"
/lab_host="p. coli BM25.8"
/note="Organ: pollen cone; Vector: Lambda TriplEx; Sii (A); Site_2: Sii (B); Immature pollen cone; Vector: Lambda TriplEx; Sii (B); Immature pollen cones were recovered by from 1 ug total RMA; Gloren and used for method ecovered by cre-lox excision in E. coli straty the lambda To c 105 g 84 t

9 others

// C 105 g 84 t

// Oches Plasmid subclones in prriplEx were
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mer: 5; lambda TriplEx2 Sequencing Primer.
10cation/Ouallfiers
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/db_xref."taxon:3352"
/cione="PCO3D12"
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                                                                             Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                         AZ917057

AZ917057
                  Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Gish,W.R., Waterston,R.H. and Johnston,M.
Surveying Saccharomyces genomes to identify functional elements by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4910.ez32q08.s1 Saccharomyces paradoxus N17 genomic clone 4910.ez32q08.s1, DNA sequence.
     comparative DNA sequence analysis
                                                                                                                                         Saccharomyces bayanus.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Genetics Washington University Medical School Box 8232, 4566 Scott Ave., St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Saccharomyces paradoxus N17"
/note="Random genomic sequence "
64 c 39 g 52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Saccharomyces paradoxus"
/strain≈"N17"
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                                  1 CCGC" "CACTCGCCGTTACTA 21
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CCGC1 CACTCGCCGTTACTA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474.dhz98g11.s1 Saccharomyces unisporus NRRL Y-1556 Saccharomyces unisporus genomic clone 474.dhz98g11.s1,\ DNA sequence. AZ932421
                                                                                                                                                                                                                                                                                                          Email: mj@genetics.wust1.edu
Class: random plasmid subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
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Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                               Tel: 314 362 2735
Fax: 314 362 7855
                                                                                                                                                                                                                                                                                                                                                                             Washington University Medical School Box 8232, 4566 Scott Ave., St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cliften, P.F., Hillier, L.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces unisporus
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                                                                                   Similarity
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                                                                 Conservative
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                                                                                                                                                    /clone="474 dhz98g11.s1"
/clone_1ib="Saccharomyces unisporus NRRL Y-1556"
/note="Random genomic sequence"
84 c 43 g 66 t
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/note="Random genomic sequence "
44 c 62 g 58 t
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/db_xref="taxon:27294"
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/strain="MCYC 623-6C"
/db_xref="taxon:4931"
                                                                                                                                                                                                                                       /organism="Saccharomyces unisporus"
/strain="NRRL Y-1556 (CBS 398)"
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GSS 01-APR-2001

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                                                                                                                                                                            Saccharomyces bayanus.
Saccharomyces bayanus.
Saccharomyces bayanus
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Eukaryota; Fungi, Ascomycota; Saccharomycetanomyces.

1 (bases 1 to 319)
Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by
                                                                                                                                                                                                                                                                                                                                                                                                   4911.fd63j12.sl Saccharomyces bayanus MCYC 623-6C Saccharomyces bayanus genomic clone 4911.fd63j12.sl, DNA sequence.
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by
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AZ932397 AZ932397.1 GI:13503310
                                     Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis
Tel: 314 362 2735
                                                                                                                         Unpublished (2001) Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: random plasmid subclone
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Box 8232, 4566 Scott Ave., St. Louis
Tel: 314 362 2735
Fax: 314 362 7855
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Email: mj@genetics.wustl.edu
                      Fax: 314 362 7855
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/clone_lib="Saccharomyees unisporus NRRL Y-1556"
/note="Random genomic sequence"
78 c 60 g 71 t
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/strain="NRRL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
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                                                           Louis, MO 63110, USA
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58 CCGCTTCACTCGCCGTTACTA 78
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                          Contact: Langkjaer RB and Piskur J
Department of Microbiology
Technical University of Denmark
Building 301, DK-2800 Lyngby, Denmark
Tel: 0045 45 45 25 18
Fax: 0045 45 93 28 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: random plasmid subclone
                                                                                                                                                                                                                                                                                                          Email: imrbl@pop.dtu.dk and imjp@pop.dtu.dk Class: plasmid ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolutionary history
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Langkjaer,R.B., Nielsen,M.L., Daugaard,P.R., Liu,W. and Piskut,
Yeast chromosomes have been significantly reshaped during their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces kluyveri.
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AZ124480.1
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KU25r S. kluyveri genomic library Saccharomyces kluyveri genomic,
                                                                                      Similarity
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/clone_lib="Saccharomyces bayanus MCYC 623-6C"
/note="Random genomic sequence "
/note="Random genomic sequence "
/note="Random genomic sequence "
                                                                                                                                                        /db_xref="taxon:4934"
/clone_lib="S. kluyveri genomic library"
/note="Vector: pBR322; Partial Sau3A fragments in BamHI"
/85 c 69 g 93 t
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/strain="MCYC 623-6C"
                                                                                                                                                                                                                                    /organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651T"
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                                                                                      Score 21; DB 12; Length 330; Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 01-JUL-2000
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Search completed: October 17, 2002, Job time: 1161.22 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    Issued_Patents_NA:*
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Copyright (c) 1993 - 2002 Commun
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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                                    US-08-632-598-2

US-08-476-866-2

US-08-943-731-116

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

US-08-943-731-3

US-08-35-836C-136

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US-08-279-700-11

US-08-279-700-11

US-08-279-700-11

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US-08-279-700-13

US-08-279-700-13

US-08-279-700-13

US-08-279-700-13

US-08-279-700-12

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	 Appli 	1, Appli	148, App	144, App	148, App	148, App	148, App	148, App	53, Appl	148, App	148, App	148, App	148, App	148, App	148, App	248, App	7, Appli	A Company

ALIGNMENTS

Query Match Best Local Similarity Watches 19; Conserve US-08-632-598-2 US-08-632-598-2 sequence 2, Application US/08632598 Patent No. 5886164 TELEFAX: 822-0944 TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: TOPOLOGY: linear MOLECULE TYPE: CDI ORIGINAL SOURCE: ORGANISM: MUSA COMPUTER READABLE FORM: MEDIOW TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 16, IMMEDIATE SOURCE: CLONE: EFE GENE REFERENCE/DOCKET NUMBER: 22 TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA: CORREST DENCE ADDRESS: APPLICANT: BIRD, COLIN R APPLICANT: FLETCHER, JONATHON D TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA NUMBER (:F SEQUENCES: 50 TYPE: nucleic acid STRANDEDNESS: single APPLICATION NUMBER: US/08/632,598 FILING DATE: ZIP: 20005-3918 CITY: WASHINGTON STATE: D.C. TELEPHONE: COUNTRY: STREET: ADDRESSEE: LENGTH: 1181 base pairs E: CUSHMAN DARBY AND CUSHMAN 1100 NEW YORK AVENUE N.W. USA linear 861-3000 CDNA 16,773 223355/SEE50112/US

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Conservative

0; Mismatches

72.2%; 82.6%;

Score 16.6; Pred. No. 15;

DВ 2:

Length 1181; Indels

0; Gaps

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ACCACGACTGAGCACGCACCTTT

23

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; Sequence 20, Application US/08476866; Patent No. 5994339; GENERAL INFORMATION:
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Best Local (
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APPLICANT: BIRD, COLIN R
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
              APPLICANT:
                                               APPLICANT:
                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: EFE GENE
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
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APPLICANT:
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710: 20005-3918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: MUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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              FRIDOVICH, IRWIN OURY, TIM DAY, BRIAN J.
FOLZ, RODNEY J
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 Mismatches

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                                                                                                                                                                                                                                        Sequence 116,
Patent No. 62
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                         APPLICANT:
                                                                                            APPLICANT:
     APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                      1238 ACCTCAACTTAGCACCCACCTTT 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10079 base pairs
TYPE: ucleic acid
STRANDE.NESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-OC APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    1 ACCACGACTGAGCACGCACCTTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                                       16, Application US/08943731 6265157
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                                                                         COLIGE, ALAIN
EARLY, JAMES
KORKKO, JARMO
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                                                                                                                          PACK, MICHAEL
                                                                                                                                         SEREDA, LARISA
LARSON, ANDREA W.
                                                                                                                                                                         DELTAS, CONSTANTINOS D.
                                                                                                                                                                                        PROCKOP, DARWIN J. SPOTILA, LORETTA D
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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5086..5803
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1993
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OMBER: US 08/136,207
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                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%;
82.6%;
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Pred. No. 21;
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US-08-943-731-3/c
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                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                             APPLICANT:
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LENGTH: 686 base pairs
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES NUMBER OF SEQUENCES: 666
                                                                                                                                                                                                                                   APPLICANT:
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APPLICATION NUMBER: 1
FILING DATE: 03-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 CGAGGACTGAGCACGCAGCTCT 387
                              STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND STREET: FLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 03-OCT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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             CITY: PHILADELPHIA
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/212,322 FILING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DOYLE LEARY Ph.D., KATHRYN REGISTRATION NUMBER: 36,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CCACGACTGAGCACGCACCTTT 23
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                                                                                                                                                        ALA-KOKKO, LEENA, et al
                                                                                                                                                                                                                                                              SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
                                                                                                                                                                                              EARLY,
                                                                                                                                                                                                             COLIGE, ALAIN
                                                                                                                                                                                                                                LARSON, ANDREA W. PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215-567-2991
                                                                                                                                                                                                                                                                                                                      PROCKOP, DARWIN J.
                                                                   PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US 07/803,628
03-DEC-1991
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                                                                                                                                                                                            , JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.8%;
81.8%;
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Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 831-494 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                 FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                            SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4798 CGAGGACTGAGCACGCAGCTCT 4777
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TELEFAX: 215-567-2991
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APPLICATION NUMBER: US 08/212,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                    APPLICATION NUMBER: UFILING DATE: 01-11-93
                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                 CITY:
                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DOYLE LEARY Ph.D., REGISTRATION NUMBER: 36,5 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brookhaven National Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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Bogosian, Margaret C.
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                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
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81.8%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                        144
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                                                     US 08/148,191
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US-08-366-577-1/c
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; LOCATION: (288)..(1892)
US-09-117-860-17
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                                                                                                            Sequence 1, Application US/08366577 Patent No. 5728523
                                                                                                                                                                                                                                                                                  Best Local Similarity 85.0%; Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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Patent No. 6338955
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CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: MO PCT/JP97/04546
EARLIER FILING DATE: 1997-12-10
EARLIER APPLICATION NUMBER: JP 161462/1997
EARLIER FILING DATE: 1997-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 17; Conserv
                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: YOSHIDA, Aruto
APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: TAKEUCHI, Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: JP 332411/1996
EARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTRANSFERASE AND GENE TITLE OF INVENTION: ENCODING THE SAME FILE REFERENCE: 081356/0119
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APPLICANT: MINOWA, Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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                    APPLICANT: Vogelsteir
APPLICANT: Kinzler, K
TITLE OF INVENTION: F
TITLE OF INVENTION: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                       1950 ACAGCTGAGCACGTACCTTT 1969
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LENGTH: 821 base pairs
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   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 ACTACGACTCAGCAGGCACC 759
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                                                                        Vogelstein, Bert
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85.08;
Kenneth W.
POLYMERASE DELTA MUTATIONS IN COLORECTAL TUMORS WITH REPLICATION ERRORS
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Pred. No. 8:
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Pred. No. 72;
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US-08-366-577-1
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                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                         CURRENT APPLICATION DATA
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                           1691 CCACGACTGAGCAGGTAGCT 1672
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                                                                                                                                                                                                                                                     APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
APPLICATION NUMBER: FILING DATE: 2-JAN-
                                                                                                                                              COUNTRY:
                                                                                                                                                                   STATE:
                                                                                                                                                                           CITY: Washington
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les 17; Conserv
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TELEFAX: 202-508-9299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/366,577
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SYSTEM: PC-DOS/MS-DOS
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             PCT/US96/00005
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US-07-642-734C-1/c
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                                     NFORMATION FOR SEQ ID NO: 1:
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HYPOTHETICAL: NO
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Mcalpine, J
B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
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                                                                                       TELECOMMUNICATION INFORMATION:
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                                          TELEPHONE: 708-938-2623
                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 17-JAN CLASSIFICATION: 435
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LOCATION:
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             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Edward H. Gorman
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nucleic acid
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         base pairs
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85.0%;
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TOPOLOGY: UNKNOWN MOLECULE TYPE: DNA MOLECULE TYPE: DNA
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase 2 domain of module 1" FEATURE:
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OTHER INFORMATION: /function- *approximate span of
OTHER INFORMATION: beta-ketoacyl ACPSynthase of module
                                                 NAME/KEY: misc_feature
LOCATION: 9906..10454
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
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LOCATION:
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LOCATION: 744..1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
  LOCATION:
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LOCATION: 2250..3626
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misc_feature
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8262..9305
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5574..6125
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module 2"
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/product= ""ORF1 encoding modules 1 & 2 for 6-deoxyerythronolide B""
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; OTHER INFORMATION: ; OTHER INFORMATION: US-07-642-734C-1
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; Patent No. 5004787
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                 TOPOLOGI.
MOLECULE TYPE: DN.
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                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                        OTHER INFORMATION: /function= "gene= "eryA""
OTHER INFORMATION: /product= ""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
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STATE:
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NAME/KEY:
                                                                                  LOCATION:
                                                                                                NAME/KEY:
                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 744..6659
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STREET: Abbott I
STREET: Park Rd
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Mcalpine,
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Abbott Laboratories D377/AP6D-2 One Abbott
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78.3%;
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                                                                                                                              /function= "APPROXIMATE SPAN OF MODULE 1"
/label= FUNCTION
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Pred. No. 1.3e+02;
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US-08-781-891-209
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                                                                                                         RESULT 12
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                                            Sequence 209, Application US/08781891 Patent No. 6090620
                                                                                                                                                                                                                                                          Best Local Similarity 78.3
Matches 18; Conservative
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GENERAL INFORMATION:
APPLICANT: Fu, Yi
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LOCATION:
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78.3%;
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APPLICANT: APPLICANT:

Fu, Ying-Hui Yu, Chang-En Oshima, Junko Mulligan, John T.

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Db 49944 ACCATGGCTGAGCATGCATCTCT 49966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 650, Application US/08943731 Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 209:
                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                         APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: "" scattle
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                                                     COUNTRY: USA
ZIP: 19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 78.3%; tes 18; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   COMPUTER:
                                                                                               STATE:
                                                                                                                               STREET:
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/781,891 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                            PHILADELPHIA
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                                                                                                                                          E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
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                                                                                                                                                                                                                                                                                                            COLIGE, ALAIN
                                                                                                                                                                                                                                                                                                                                              SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
LARSON, ANDREA W.
                                                                                                                                                                                                                                                                                                                           PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                  PROCKOP, DARWIN J
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E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 622-4900
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Pred. No. 1.6e+02;
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; OTHER INFORMATION: any n or Xaa = Unknown US-09-230-944-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09230944; Patent No. 6277380
                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
   Best Local Similarity
                  Query Match
                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 0216-0407P
CURRENT APPLICATION NUMBER: US/09/230,944
CURRENT FILING DATE: 1999-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: UEDA, Shigeharu
APPLICANT: WATANABE, Michiko
APPLICANT: KAMANISHI, Hitomi
TITLE OF INCANTION: Measles Virus Mutant Antigen and Gene Coding for the
                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 9-184285 JAPAN EARLIER FILING DATE: 1997-06-04 NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/JP98/02481 EARLIER FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Same
                                                                                           OTHER INFORMATION: Attenuated measles virus NA strain FEATURE:
                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)..(1851)
                                                                                                                                                                           ORGANISM: Measles virus FEATURE:
                                                                                                                            FEATURE:
                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                              LENGTH: 1854
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TELECOMMUNICATION INFORMATION: 215-965-1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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 64.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
Score 14.8; DB 4; Length 1854; Pred. No. 1.3e+02;
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Pred. No. 68;
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Matches

16;

Conservative

0;

Mismatches

Indels

0;

Gaps

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-279-700-3
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,700
FILING DATE:
CLASSIFICATION & 435
PRIOR APPLICATION NUMBER: US/07/866,033A
FILING DATE: 19920408
CLASSIFICATION NUMBER: 29,786
CLASSIFICATION NUMBER: 29,768
REPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 435
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (703)683-4109
TELEFAN: (703)683-4109
TELEFAN: 899149
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1874 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
Search completed: October 17, 2002, 08:52:21 Job time: 65.7111 secs
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                                                                                                                                                                     Query Match 64.3%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROTA, Jennifer S.
APPLICANT: BELLINI, WILLIAM J.
TITLE OF INVENTION: WILD-TYPE MEASLES VIRUS GLYCOPROTEINS:
TITLE OF INVENTION: VACCINE AND DETECTION METHOD THEREFOR NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                             3 CACGACTGAGCACGCACC 20
||| |||||||||| |||||
760 CACAACTGAGCATGCACC 777
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740 CACAACTGAGCATGCACC 757
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CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
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21..1874
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                                                                                                                                                                                     Score 14.8; DB 1;
Pred. No. 1.3e+02;
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                                                                                                                                                                   Indels
                                                                                                                                                                   0;
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AUTHORS Brown,S., Rouse,G., Hutchings,P. and Colgan,D.

TITLE Direct Submission
JOURNAL Submitted (13:SEP-1999) Evolutionary Biology, Australian Museum, 6

FEATURES Submitted (13:SEP-1999) Evolutionary Biology, Australian Museum, 6

Location/Qualifiers
Source Location/Qualifiers

Source 1.307
/organism="Mesochaetopterus sp. AMW22402"
/specimen_voucher="AMW22402"
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linear

INV 20-007-1999

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REFERENCE
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                                                                                                                          Submitted (13-SEP-1999) Evolutionary Biology, Australian Museum, 6 College Street, Sydney, NSW 2000, Australia
                                                                                                                                                                                                                    Assessing the usefulness of histone H3, U2 snRNA and 28S rDNA in analyses of polychaete relationships Aust. J. 2001. 47 (1999) In press
                                                                                                                                                                                                                                                                                                                           Amphiglena terebro
Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyophthalmus pictus 28S ribosomal RNA gene, partial sequence AF185171
                                                                                                                                                                                                                                                                              Brown, S., Rouse, G., Hutchings, P. and Colgan, D.
                                                                                                                                                                                                                                                                                                                                                                                                         AF185150.1 GI:6013331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-SEP-1999) Evolutionary Biology, Australian Museum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                   Direct Submission
                                                                                                                                                                                 Brown, S., Rouse, G., Hutchings, P. and Colgan, D.
                                                                                                                                                                                                                                                                                                               Sabellida; Sabellidae; Amphiglena
                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphiglena terebro 28S ribosomal RNA gene, partial sequence
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                               /organism="Amphiglena terebro"
/specimen_voucher="AMW21360"
/db_xref="taxon:104683"
/note="D1 expansion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="28S ribosomal RNA"
84 c 97 g 59 t
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/specimen_voucher="AMW10095"
/db_xref="taxon:104727"
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2 (b
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                                                                                                                                                                                                                                                         AF185163 307 bp DNA linear INV 20-00 Mesochaetopterus sp. AMW22402 28S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assessing the usefulness of histone H3, U2 snkNA and 28S rDNA in analyses of polychaete relationships Aust. J. Zool. 47 (1999) In press
             analyses of polychaete relationships Aust. J. Zool. 47 (1999) In press
                                                  Brown, S., Rouse, G., Hutchings, P. and Colgan, D
Assessing the usefulness of histone H3, U2 snl
                                                                                                         Eukaryota; Metazoa; Annelida; Polychaeta; Palpala; Canalipalpala; Spionida; Chaetopteridae; Mesochaetopterus.
                                                                                                                                              Mesochaetopterus sp. AMW22402
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                                                                                                                                                             Mesochaetopterus sp. AMW22402.
                                                                                                                                                                                                    AF185163.1 GI:6013344
                                                                                                                                                                                                                                         sequence.
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 (bases 1 to 307)
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81 c 97 g 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycera tridactyla"
/specimen_voucher="AMW196835"
/db_xref="taxon:104710"
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79 c 92 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="D1 expansion region"
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snRNA and 28S rDNA in

INV 20-0CT 1999

Gaps

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RESULT 10
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                                                                      CCGCTTCACTCGCCGTTACTAG
                                                                                                  CCGCTTCACTCGCCGTTACTAG 22
    AF265622
                                                                                                                                                                                                                                                                                                           Submitted (23-JAN-2001) Laboratoire de Biologie des Invertebres Marins et Malacologie, Institut de Systematique FR 1541, Museum National d'Histoire Naturelle, 43 rue Cuvier, Paris 75005, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nautilus 108 (supplement 2), 122-140 (1994)
2 (bases 1 to 295)
Dayrat,B., Tilller,A., Lecointre,G. and Tilller,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tillier,S., Masselot,M., Guerdoux,J. and Tillier,A. Monophyly of major Gastropod taxa tested from partial 28S rRNA sequences, with emphasis on Euthyneura and hot vent limpets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF339505 AF358804
AF339505.1 GI:13445764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aplysia depilans 28s ribosomal AF339505 AF358804
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    Tillier,S., Masselot,M., Guerdoux,J. and Tillier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular phylogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New clades of euthyneuran gastropods (Mollusca) from 28S rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aplysia depilans
Aplysia depilans
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                                                                                                                                Conservative
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                                                                                                                                                                                                                                             /organism="Aplysia depilans"
/db_xref="taxon:76186"
<1. .>295
                                                                                                                                                                                                  /product="28S ribosomal RNA"
76 c 91 g 55 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /country="France: Antifer Harbour" <1. .>283
                                                                                                                                                                                                                                 /note="D1 domain"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="24S large subunit ribosomal RNA'
53 c 89 g 63 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:150676"
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/isolate="Cons3"
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Eukaryota; Metazoa; Cnidaria; Anth
Eukaryota; Metazoa; Cnidaria; Anth
Caryophylliina; Caryophylliidae; C
1 (bases 1 to 304)
Romano, S.L. and Cairns, S.D.
Molecular phylogenetic hypotheses
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22; Conserv
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22; Conserv
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2 (bases 1
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Romano, S.L. and Cairns, S.D.
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                          Conservative
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/db_xref="taxon:123772"
<1. .>303
                                                                                              /product="28S ribosomal RNA"
68 c 92 g 64 t
                                                                                                                          /db_xref="taxon:130053"
<1. .>304
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Caryophyllia inornata 28S ribosomal RNA gene, partial sequence. AF265642
AF265642.1 GI:8980731
                                                                                                                                                                                                                                                      Romano,S.L. and Cairns,S.D. Direct Submission Submitted (09-MAY-2000) Laboratory of Molecular Systematics, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0163, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAY-2000) Laboratory of Molecular Systematics, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0163, USA
                                                                                                                                                                                        /organism="Caryophyllia inornata"
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                                                                                                                                                                                         Nature 3:
95327188
                                                                                                                                                                                                     Ribosomal DNA phylogeny of the major
the evolution of myriapods
Nature 376 (6536), 165-167 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reassessing evolutionary relationships of scleractinian corals Coral Reefs 15, 1-9 (1996)
3 (bases 1 to 222)
                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (09-AUG-1995) M. Friedrich,
                                                                                                                                                                                                                                                                                                                                                                                                         Tubifex sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TS28S259 259 bp
Tubifex sp. gene for 28S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-JUL-1996) Biochemistry and Molecular Biology, Cook University, Townsville, Queensland 4811, Australia Location/Qualifiers
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                                                                                                                                                                                                                                                          Friedrich, M. and Tautz, D.
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                                                                                                                                                                                                                                                                                       Muenchen, Luisenstr. 14, D-
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Tubificina; Tubificidae; Tubifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                      28S ribosomal RNA; 28S rRNA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       X90690.1 GI:1067238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x90690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Veron, J.E.N., Odorico, D.M., Chen, C.A. and Miller, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95392827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, C.A., Odorico, D.M., ten Lohuis, M., Veron, J.E. and Miller, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Astrocoeniina; Pocilloporidae; Seriatopora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seriatopora hystrix.
Seriatopora hystrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U65520.1 GI:1553147
                                                                                                                                                                                                                                                                       (bases 1 to 259)
                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 259)
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               54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
               D
           /gene="28S rRNA"
75 c 84
                                                                                                                            /organism="Tubifex sp.
/db_xref="taxon:44764"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="28S ribosomal RNA"
53 c 68 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Seriatopora hystrix"
/db_xref="taxon:51070"
                                                         /product="28S ribosomal RNA"
                                                                            /gene="28S rRNA"
                                                                                                         /dev_stage="adult"
                                                                                                                                                                      Location/Qualifiers
                                               . 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No.
             84 g
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             46 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA (partial; 259 bp).
                                                                                                                                                                                                                                         extant arthropod
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nchen, FRG
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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ORGANISM
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Best Local Similarity
                TITLE
                                        AUTHORS
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Best Local Similarity
  JOURNAL
                                                                   JOURNAL
                                                                                                                                    AUTHORS
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U75861
                                                                                       Eukaryota; Fungi; Basidiomycota; environmental samples.

1 (bases 1 to 283)

Guillou,L., Nezan,E., Cueff,V., Erard-Le Denn,E., Cambon,M.-A.,
Gentien,P. and Barbier,G.

Semi-nested PCR detection of three toxic dinoflagellate general
(Alexandrium, Dinophysis, and Gymnodinium) in sea water column and
Direct Submission Submitted (02-NOV-2000) DRV VP CMM, IFREMER,
                         Guillou,L., Nezan,E., Cueff,V.,
Gentien,P. and Barbier,G.
                                                                                                                                                                                     uncultured basidiomycote Cons3
                                                                                                                                                                                                                              gene, partial sequence. AF318260
                                                                                                                                                                                                                                                      Uncultured basidiomycote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-OCT-1996) Biology, U
3020, Victoria, BC V8W 3N5, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theodoxus
                                                                Unpublished
                                                                                                                                                                        uncultured basidiomycote Cons3
                                                                                                                                                                                                                 AF318260.1 GI:13236258
                                                                                                                                                                                                                                                                     AF318260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular investigation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McArthur, A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theodoxus
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                                                                             sediment from French coasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McArthur, A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thesis, University of Victoria, Canada. (1996) 2 (bases 1 to 276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vent gastropods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [heodoxus
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                                                      (bases 1 to 283)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:55034"
/dev_stage="-"-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="28S ribosomal RNA gene"
76 c 91 g 48 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
<1. .>276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.
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100.0%;
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28S ribosomal RNA
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Pred. No. 20;
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Pred. No.
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                                       Erard-Le Denn, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
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  .P
 70, Brest 29280,
                                        Cambon, M.
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E64938/c
   REFERENCE
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                                                                                             VERSION
                                                                                                           ACCESSION
                                                                                                                           DEFINITION
                                                                                                                                                      CSU69678/c
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                                                                                                                                           FOCUS
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                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                  59 CCGCTTCACTCGCCGTTACTAG
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OS Nico
PN JP 1
PD 24-N
PF 19-M
                                                                                                                      CSU69678 219 bp DNA linear INV Cerianthus sp. 28S ribosomal RNA gene, partial sequence
Ceriantharia; Cerianthidae; Cerianthus. 1 (bases 1 to 219)
                                               Cerianthus
                                                             Cerlanthus
                                                                                           U69678.1 GI:1617542
                                                                                                             U69678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence of gene perticipating
                         Eukaryota; Metazoa; Cnidaria; Anthozoa; Ceriantipatharia;
                                                                                                                                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N5/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIEGRIED KIDOROUSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana 1 (bases 1 to 218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E64938.1 GI:13017969
JP 1999318477-A/70.
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PETER HELMUTO SCHREIER, CHRISTINE GARBERS, GREGOR LANGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum
JP 1999318477-A/70
                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1999 JP 1999075762
25-MAR-1998 DE 19813048
                                                                                                                                                                                                                                                                                                                                                      ۵
                                                                                                                                                                                                                                                                                                                                                   /organism="Nicotiana tabacum"
/db_xref="taxon:4097"
43 c 65 q 42 t
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                             sp.
                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism='Nicotiana
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                                                                                                                                                                                                                                                                                          Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB
Pred. No. 21;
                                                                                                                                                                                                                                                                             Mismatches
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LOCUS

Scriatopora hystrix 28S ribosomal RNA gene, partial sequence, U65520

INV 08-00T-1996

ACCESSION DEFINITION

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RESULT 5
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AUTHORS
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069690
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Chen, C.A., Odorico, D.M., ten-Lohuis, M., Veron, J.E. and Miller, D.J.
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Chen, C.A., Odorico, D.M., ten-Lohuis, K., Veron, J.E. and Miller, D.J.
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Chen,C.A., Odorico,D.M., ten-Lohuis,M., Veron,J.E. and
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                                                                                                                                                                                                                                                                                                                         Submitted (06-SEP-1996) Biochemistry and Molecular Biology, James
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Compugen Ltd
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AX014514/c
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                                                                                             ORGANISM
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                                                            AUTHORS
                                                                                                                                                                                         source
                                                                   Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                   1 (bases 1 to 218)
Kiedrowski, S.D., Garbers
Cdna sequences of genes
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Sequence 70 from Patent
AX014514
AX014514.1 GI:10040789
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                                       EP 0953640-A 70 03-NOV-1999;
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      /organism="Nicotiana tabacum"
/db_xref="taxon:4097"
                          Location/Qualifiers
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                                                   Garbers,C.D., Langen,G.D. and Schreier,P.H. f genes involved in the induction of resistance
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AF358918
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LOUZERRN5
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AF185150 Amphiglen
AF185153 Mesochaet
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AF185165 Sigalion
AF185167 Euryyhoe
AF185164 Paralepid
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AF300719 Salal roo
U43472 Ophiobolus
U43471 Ophiobolus
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AF261555 Protubera
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U45828 Candida hal
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE KEYWORDS SOURCE RESULT 1 AF042820/c LOCUS ACCESSION VERSION FEATURES DEFINITION JOURNAL ORGANISM Direct Submission Submitted (14-JAN-1998) Department of Microbiology, Inje University, Obangdong 607, Kimhae 621-749, Korea AF042820 Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.

1 (bases 1 to 712)

Lee,S.W., Park,C.G. and Park,Y.S.

24S ribosomal RNA sequence analysis of dinoflagellates isolated from red-tide in southern coast of Korea Heterosigma akashiwo. Heterosigma akashiwo Unpublished AF042820.1 Heterosigma akashiwo 24S AF042820 Lee, S.W., Park, C.G. and Park, Y.S. (bases 1 to 712) Location/Qualifiers
1. .712 GI:2827390 712 bp DNA linear PLK 01-FEB-1998 large subunit ribosomal RNA-game_Bartial

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                           Eukaryota: stramenopiles; Raphidophyceae; Heterosigma.

1 (bases 1 to 715)

Tyrrell, J.V., Scholin, C.A., Bergquist, P.R. and Bergquist, P.L.

Detection and Enumeration of Heterosigma akashiwo and Fibrocapsa japonica (Raphidophyceae) Using rRNA-Targeted Oligonucleotide
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Eukaryota; stramenopiles; Raphidophyceae; Heterosigma
1 (bases 1 to 713)
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Seattle, WA 98112, USA
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/product="large subunit ribosomal RNA"
148 c 210 g 190 t
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/db_xref-"taxon:2829"
/note="isolated from red-tide sea water in Masan Bay,
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/strain="CCMP-452"
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Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
Phylogeny of the Raphidophytes Based on Large-Subunit rRNA Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.

1 (bases 1 to 715)

Tyrrell, J.V., Scholin C.A., Bergquist, P.R. and Bergquist, P.L.

Detection and Enumeration of Heterosigma akashiwo and Fibrocapsa
japonica (Raphidophyceae) Using rRNA-targeted Oligonucleotides
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Tyrrell,J.V., Bergquist,P.R.,
                                                                                                                                                                                                                                                          Submitted (03-DEC-1999) Research and Development, Aquarium Research Institute, 7700 Sandholdt Road, 95039-0628, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heterosigma sp. CAWR10.
Heterosigma sp. CAWR10
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Tyrrell, J.V., Bergqu
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Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
                                                                                                                                                                                                                                                                                                                                                                                   sequences
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                                                            sequence presented in GenBank Accession Number AF210741"
/product="large subunit ribosomal RNA"
1 148 c 212 g 189 t
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/product="large subunit ribosomal RNA"
| 148 c 212 g 189 t
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/db_xref="taxon:2829"
                                                                                                                   /note="D1 and D2 domains; similar to Heterosigma akashiwo
                                                                                                                                                   /note="similar to Heterosigma akashiwo sequence AF210741"
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Du,F., Wohldmann,P. and McGrane,B.
The sequence of Homo sapiens PAC clone RP5-1044J9
                                                              Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                             1 (bases 1 to 126149)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-AUG-2001) Biochemistry, University of Antwerp, Universiteitsplein 1, Wilrijk 2610, Belgium
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290. .447
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899 c 1142 g 1017 t
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/db_xref="taxon:2829"
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Submitted (11-JAN-1999) Genome Sequencing Center, Washington
Submitted (11-JAN-1999) Genome Sequencing Center, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
3 (bases 1
                                                                                                                                                                Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On May 5, 1999 this sequence version replaced gi:4337277.
                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                  5 (bases 1 to 126149) Waterston, R.
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Center project name: H_DJ1044J09
                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                             Contact: sapiens@watson.wustl.edu
                                                                        Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                 -- Genome Center
                           Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc University Genome Sequencing Center. For additional information The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington

SOURCE INFORMATION:

one male donor (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute is from

VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION: The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

position 1 of RP5-1044J9;

FEATURES source start of this clone is at base end is at 126149 of RP5-1044J9 Location/Qualifiers

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/db_xref="taxon:9606" /map="7p14-p12" /clone="RP5-1044J9" /chromosome="7"

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misc_feature
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11044. .11411
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1590. .1602
                      /note="similar to EST R72787 (NID:g846819) yj91h09.r1" 17447. .17750
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    /note="similar to Mus musculus EST AA170256 (NID:g1748794)
                                                                 /note="similar to EST R72787 (NID:g846819) yj91h09.r1"
17447. .17748
                                                                                                                      /note="similar to Mus musculus EST AA575218 (NID:g2349844)
vh19a01.r1"
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AUTHORS
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AL627202/c
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                                                                                                                                              Submitted (05-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                              AL627202 169710 bp DNA linear HTG 07-NOV-HOMO sapiens chromosome 1 clone RP11-174P23, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.
Center project name: bA174P23
                                Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                On Oct 30, 2001 this sequence version replaced gi:16501251
                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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25650. .26548
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17447. 17751
/note="similar to Mus musculus EST AA575218 (NID:q234v844)
vh19a01.rl"
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25461. .25486
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22114. .22213
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24954. .25460
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24524. .24597
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87.0%;
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7. .25557
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Pred. No. 69;
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HTG 07-NOV-2001

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FEATURES
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 165366 bases at least Q40
Consensus quality: 167034 bases at least Q30
Consensus quality: 167987 bases at least Q20
Consensus quality: 167987 bases at least Q20
Insert size: 168610; sum-of-contigs
Insert size: 17230; 12,6% error; agarose-fp
Quality coverage: 5.03x in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently * consists of 12 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coverage: 5.15x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117991: contig of 2065 bp in length
117991 118090: gap of 100 bp
118091 129051: contig of 10961 bp in length
129052 129151: gap of 100 bp
129152 15951: gap of 100 bp
155348 155447
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77652 77751: 1
77752 8332
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48866 77651: contig of 28786 bp in length
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89477 95053: contig of 5577 bp in length
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                         /note="assembly_fragment:02114
fragment_chain:2"
95154, .115825
/note="assembly_fragment:03342
                                                                                                                                                                                              fragment
                                                                                                                                                                                                /note="assembly_fragment:02530
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                              fragment.
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                                                                                                                      /note="assembly_fragment:01668
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:02971
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:03428
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                           /note="assembly_fragment:02451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:00723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-174P23"
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contig of 14263 bp in length
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                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 sequencing vector: M13; M77815; 1% of reads sequencing vector: plasmid; LO8752; 98% of reads Chemistry: Dye-terminator Big Dye; 100% of reads consensus quality: 188643 bases at least Q40 Consensus quality: 188754 bases at least Q30 consensus quality: 188773 bases at least Q30 consensus quality: 188773 bases at least Q30
                                                * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                             Insert size: 188839; sum-of-contigs
Insert size: 187990; 6.8% error; agarose-fp
Quality coverage: 11.94x in Q20 bases; sum-of-contigs Quality
coverage: 12.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 4, 2002 this sequence version replaced gi:16501196.
                             * as soon as it is available and the accession number will
                                                                                                                          * consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: bA203F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL592114 188930 bp DNA linear HTG 03-JAN Homo sapiens chromosome 1 clone Rp11-203F10, *** SEQUENCING IN
                                                                                                                                                                                * NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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be preserved.
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fragment_chain:2"
129152. .155347
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fragment_chain:2"
118091..129051
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Pred. No. 6
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34047: contig of 34047 bp in length

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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson, Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
                                                                                                                      Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2001 this sequence version replaced gi:14190724. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamazares, R., Landers, T., Lehoozky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., McPheeters, R., Maldrim, J., Menaus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Connor, T., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Rosetti, M., Roy, A., Santos, R., Schupback, R., Schup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 197083)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                     Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo.A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
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                                                                                                                                                                                                                                                                               Submitted (29-MAR-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                      Zainoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus chromosome 6, clone RP23-103L13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iliev,I., Johnson,R., Jones,C., Karatas,A.,
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ture 34148. 188330
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Center: Whitehead Institute/ MIT Center for Genome Research
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/clone_lib="RPCI-11.1"
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/db_xref="taxon:9606"
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188930: con
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87.0%;
                                                                                                                                                                                                                                                                                                                                                                      Zembek, L., Zimmer, A. and Zody, M.
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contig of 154783 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197083 bp
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WORKING DRAFT
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78044 92354: contig of 14311 bp in length 92355 92454: gap of 100 bp 101645 101743: gap of 100 bp in length 101644 101743: gap of 100 bp in length 112044 112143: gap of 100 bp in length 112044 112143: gap of 100 bp 112144 137609: contig of 25466 bp in length 137610 137709: gap of 100 bp 106876: contig of 23167 bp in length 137610 1376976: contig of 23167 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
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Assembly program: Phrap; version 0.96073
Consensus quality: 186756 bases at least Q40
Consensus quality: 191296 bases at least Q30
Consensus quality: 193282 bases at least Q20
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15/710 160876: contig of 23167 bp in 160877 160976: gap of 100 bp 160977 179898: contig of 18922 bp in 79899 179998: gap of 100 hr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 190000; agarose-fp
Insert size: 194683; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30981 37313: contig of 6333 bp in length
37314 37413: gap of 100 bp
37414 42184: contig of 4771 bp in length
42185 42284: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2494
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19364 19463: gap of 100 bp
19464 24944: contig of 5381 bp in length
24845 24944: gap of 100 bp
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16335: contig of 3957 b
16336 16435: gap of 100'
16436 19363.
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4611 71
7192 7291:
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2514 2613: gap of 10
2614 3159: contin
3160 anen
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48206: contig of 5922 bp in length
48306: gap of 100 bp
58278: contig of 9972 bp in length
58378: gap of 100 bp
69851: contig of 11473 bp in length
59951: gap of 100 bp
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4510: con
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2513: con
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contig of 546 bp in length
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SOURCE

TITLE

KEYWORDS VERSION Locus

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16436. .19363
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12379. .16335
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9130. .12278
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42285. 48206
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179999. .197083
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101744. .112043
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87.0%;
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                                                                                                                      Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Apr 20, 2000 this sequence version replaced gi:5836167.
                                                                                                                                                                                                               University School of Medicine, 4444 Forest Park Parkway, St. Mo 63108, USA
7 (bases 1 +- 2000)
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Reitz,L., Stoneking,T.
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Mammalia; Eutheria; Primates; Catarrhini;
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Center project name: H_NH0499D05
                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
                                                                     Center: Washington University Genome Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

COMMENT

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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= This sequence was finished as follows unless otherwise noted:

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actual start of this clone is at base actual end is at base position 214025
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPPING INFORMATION:
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VECTOR: pBACe3.6
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2290. .2312
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2138. .2152
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/clone="RP11-499D5"
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                                           /rpt_family="MER2_type"
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AC007908/c LOCUS DEFINITION

227856 bp DNA linear HTG 25 Homo sapiens chromosome 16 clone RP11-499D5, WORKING DRAFT SEQUENCE, 30 unordered pieces.

HTG 25-APR-2001

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RESULT 11
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3951. .3971
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3796. .3821
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4385. .4392
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4044. .4072
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7184. .7418
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4858. .4881
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4226. .4276
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                                                                                                                                                            /rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                     Estimated insert size: 218590; agarose-fp estimation
Estimated insert size: 224956; sum-of-contigs estimation
Quality coverage: 4.43 in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.3 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 184734 bases at least Q40 Consensus quality: 201642 bases at least Q30 Consensus quality: 209314 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Institute, Los Alamos National Laboratory, MS M888, Alamos, NM 87545, USA
On Jul 13, 2000 this sequence version replaced gi:7211873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R., Camberly,K., Han,C. and Deaven,L.
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Center clone name: RPCI-11_499D5
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DOE Joint Genome Institute.
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                    Genome duplications and other features in 12 mb of DNA sequence from human chromosome 16p and 16q Genomics 60 (3), 295-308 (1999)
                                                          Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R., Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L. Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S., Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
                                                                                                                                                                                                           HUACUUZU41 234542 bp DNA linear PRI 23-NOV-19
Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.
ACO02041
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Cronin, L.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail address: mdadams@tigr.org. The bac location is on chromosome BAC clone is located on human chromosome 16p11.2 The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.orn1.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/ chris/GENSCANW.html) searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medical Center Dr., Rockville, MD 20850, USA
On Oct 30, 1997 this sequence version replaced gi:2570252.
Address all correspondence to: Mark Adams The Institute for Genomic
Research 9712 Medical Center Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Center Dr., Rockville, 6 (bases 1 to 234542)
Adams, M.D. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-OCT-1997) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA 5 (bases 1 to 234542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-APR-1997) The
                                                                                                                                                                                                                                                                                                                                                                                                                            without pepetide homolgy having spliced EST hits are termed 'unknown protein'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/)
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7 (bases 1 to 234542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAR-1998) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-SEP-1998) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the Human gene index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html). A gene with homolgy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence against a peptide database,
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                                                                                                                                                                                                                                             /pseudo 59641.
                                                                                       complement(128248. .129149)
/gene="A-17E1.2"
   /note="42649, sWSS4047, Chr. 7, Homo sapiens"
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                                   /pseudo
132476. .132730
                                                                                                                            /note="32826, A002D07, Chr. -,
/db_xref="dbSTS:G19948"
                                                                                                                                                                                                                                                                              /gene="A-17E1.9"
                                                                                                                                                                                                                                                                                                   36147.
                                                                                                                                                                                                                                                                                                                   /map="16p11.2"
/clone="A-17E1"
                                                                                                                                                                                                                                                                                                                                                      /chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                        /note="pseudogene"
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                                                                                                                                                                                                                        /gene="A-17E1.1"
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Unpublished
3 (bases 1
                                 Du, F., Hadkenson, W., Elliott, G. and Richards, M. Du, F., Hadkenson, W., Elliott, G. and Richards, M. The segmence of Homo sapiens BAC clone RP11-327F6
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                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                              1 (bases 1 to 215359)
Sulston, J.E. and Waterston, R.
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228452.
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190412.
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50172 c 50664 g
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160622. 160753
/mote="32826, A002D07, Chr. -, Homo sapiens"
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163896. 164027
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note="42758, D1S1053, Chr. -, Homo sapiens"

/db_xref="db578:G28812"

137107. 137238
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/gene="A-17E1.10"
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149776. .149953
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/gene="A-171E.6"
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                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            GI:16756348
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87.0%;
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Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-NOY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA on Nov 7, 2001 this sequence version replaced gi:13431146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis McPherson and information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RP11-434B12; the clone sequenced to the right is AC051646. Actual start of this clone is at base position 1 of RP11-327F6; actual end is at base position 215359 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restriction digest.
                                                                                                                                                                                                                                                                                                                                represented by sequence derived from PCR on BAC DNA
                                                                                                                                                                                                                                                                                                                                                    The sequence H_NH0327F06 from base positions 115714 to 115728 is
                                                                                                                                                                                                                                                                                                                                                                                               RP11-327F6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://bacpac.med.buffalo.edu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------Summary Statistics
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                     /rpt_family="Alu"
2744. .3066
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846. .1142
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473...757
                                                                                                                                             164.
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/chromosome="2"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                               /clone="RP11-327F6"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
  /rpt_family="MER2_type"
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8207. .8227
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19700. .19759
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8476. .8607
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27985
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17498. .17825
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14307. .15160
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14106. .14201
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11462. .11768
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31839
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31406
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28752
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22657
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20576. .20600
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20267. .20410
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                                         /rpt_:
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32707
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29211. .29265
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24055. .24075
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22731. .22752
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20601. .20657
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  /~pt_family="Alu"
34685. .34962
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                                                                                                                                                                                                                                                                                                                                                        _family="Mariner"
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5. .28215
                                                      family="L1"
                                                                                                                                       family="L1"
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                                                                                                  family="MaLR"
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                                           .34373
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                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-JUL-1999) Laboratoire IECH - Institut de Genetique et Microbiologie Universite Paris XI 91400 ORSAY - FRANCE & Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE & UGM - Centre d'Etudes du Bouchet BP3 91710 Vert le Petit - FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens genomic region containing hypervariable minisatellites chromosome 8[8g24.3] of Homo sapiens.
                                                                                                                                          BP 191
                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petit, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                             Web : www.genoscope.cns.fr)
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                                                                                                                                    ted (05-JUL-1999) Genoscope - Centre National de Sequencage 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                      Submission
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45073. .45094
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             /organism="Homo sapiens"
                                                                        Location/Qualifiers
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36033. .36204
                                                                                                                                                                                                                                                                                                                                                                                                                                                Vico, V., Brottier, P. and Vergnaud, G.
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39472. .39493
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6. .48703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Aug 11, 2001 this sequence version replaced gi:7767808 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tirrell, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, F.
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Change, C., Collins, C., Collins, C., Cooke, F., 
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Homo sapiens, clone RP11-225D16
Unpublished
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Homo sapiens clone RP11-225D16, WORKING DRAFT SEQUENCE, 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                Center project name: L5810
Center clone name: 225_D_16
Center clone summary Statistics
                                                 Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 0.960731
Consensus quality: 184156 bases at least 040
                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
Consensus quality: 190337 bases at least Q30 Consensus quality: 193088 bases at least Q20
                                                                                                                   Sequencing vector: Plasmid; n/a; 51% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                         Sequencing vector: M13; M77815; 49% of reads
                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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8558 c 86
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/chromosome="8"
/clone="CEB42"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- Genome Center
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Pred. No. 1.8e+02;
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Castle, A.,

CNS00YVE

Matches

FEATURES

REFERENCE

AUTHORS

JOURNAL

REFERENCE

JOURNAL AUTHORS SOURCE

KEYWORDS

VERSION ACCESSION

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Insert size: 170000; agarose-fp
Insert size: 194664; sum-of-contigs
Quality coverage: 12.6 in Q20 bases; agarose-fp
Quality coverage: 11.0 in Q20.

* NOTE: This is a 'working draft' sequence. It currently
consists of 32 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
as soon as it is available and the accession number will
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                                                                                13624 14303; contig of 680 bp in le
13624 14403; gap of 100 bp
14404 11505; contig of 652 bp in le
15056 15155; gap of 100 bp
15156 15778; contig of 623 bp in le
15779 15878; gap of 100 bp
15879 16229; contig of 351 bp in Le
16230 16329; gap of 100 bp
16330 16387; contig of 558 bp in le
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13624 1430
14304 14403:
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61 20742: contig of 1182 bp
43 20842: gap of 100 bp
43 21533: contig of 691 bp
34 21633: gap of 100 bp
34 22342: contig of 709 bp
34 22342: gap of 100 bp
36 22442: gap of 100 bp
43 2311: contig of 669 bp
12 23211: gap of 669 bp
12 23211: gap of 661 bp
12 23212: contig of 681 bp
                                                                                                                           35847: gap of 100 bp 36927: contig of 1080 bp in length 37027: gap of 100 bp 42128: contig of 5101 bp in length
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3947: contig of 802 bp in 1
34047: gap of 100 bp
35747: contig of 1700 bp in
35847: gap of 100 bp
                                                                         51023:
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30221: contig of 868 bp in length
30321: gap of 100 bp
31453: contig of 1132 bp in length
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23992: gap of 100 bp
24854: contig of 862 bp in length
24954: gap of 100 bp
26017: contig of 103 bp in length
26117: gap of 100 bp
26128: contig of 211 bp in length
26238: contig of 211 bp in length
26238: gap of 100 bp
27272: contig of 844 bp in length
27372: gap of 100 bp
27372: gap of 100 bp
28385: gap of 100 bp
28385: contig of 846 bp in length
28385: gap of 100 bp
28223: contig of 868 bp in length
28385: gap of 100 bp
28233: gap of 100 bp
28233: gap of 100 bp
228: gap of 100 bp 5
50923: contig of 8695 bp in length
023: gap of 100 bp
76863: contig of 25840 bp in length
963: gap of 100 bp
123889: contig of 46926 bp in length
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